

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 11:07:47 ; Search time 4744 Seconds
(without alignments)
10971.708 Million cell updates/sec

Title: US-10-069-541-5
Perfect score: 1743
Sequence: 1 atggctttccatgtggaagg.....ctgaagataatttacagtga 1743

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
	No.	Score	Match	Length	ID	
	1	1473	84.5	1743	29	AY413298 Homo sapi
	2	1463	83.9	1743	29	AY413299 Pan trogl
	3	1375	78.9	4097	11	AK053063 Mus muscu
	4	1375	78.9	4306	11	AK034415 Mus muscu
	5	1156.2	66.3	1743	29	AY413300 Mus muscu
	6	518.8	29.8	672	29	AG157499 Pan trogl
	7	472.2	27.1	707	14	CD350164 UI-M-FY0-
	8	462.8	26.6	669	13	BY727598 BY727598
	9	404	23.2	516	10	BE233479 139685 MA
	10	329.8	18.9	650	10	BB626260 BB626260
	11	312.8	17.9	541	10	AW668962 111664 MA
	12	290	16.6	675	13	BY729567 BY729567
	13	274.2	15.7	524	10	BE723927 198406 MA
	14	263.2	15.1	800	9	AL669749 AL669749
	15	225.8	13.0	549	13	BW274870 BW274870
	16	212.4	12.2	1037	9	AL666817 AL666817
	17	210	12.0	941	14	CD360297 AGENCOURT
	18	209.2	12.0	641	12	BI630566 RH59836.5
	19	207.4	11.9	640	12	BI629504 RH58381.5
	20	205.2	11.8	658	12	BM629925 170006875
	21	203.2	11.7	652	10	BB626456 BB626456
	22	193.6	11.1	583	13	BW277281 BW277281
	23	192.6	11.0	605	13	BQ829470 LL6in2176
	24	186.4	10.7	624	12	BJ122485 BJ122485
	25	183	10.5	681	14	CD306544 StrPu691.
	26	178.6	10.2	565	12	BJ125564 BJ125564
	27	177.4	10.2	576	14	CB391304 OSTF149A8
	28	176.6	10.1	310	9	AL918603 AL918603
	29	166	9.5	604	9	AU199794 AU199794
	30	163.4	9.4	500	9	AV994375 AV994375
	31	163.2	9.4	555	12	BJ117801 BJ117801
	32	158.4	9.1	646	9	AB078155 AB078155
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	35	153	8.8	584	12	BJ105382 BJ105382
	36	145.2	8.3	500	12	BP186503 BP186503
c	37	134	7.7	632	28	AZ612750 1M0439J17
	38	128.2	7.4	500	12	BJ105730 BJ105730
c	39	127.6	7.3	618	28	AZ908709 RPCI-24-2
	40	121	6.9	926	29	CNS04L3J Tetraodon
c	41	117.2	6.7	525	12	BI508286 BB170004A
c	42	117.2	6.7	530	12	BI503332 BB170012A
	43	112.8	6.5	355	9	AU209671 AU209671
c	44	112.4	6.4	558	12	BI507950 BB170010A
c	45	108	6.2	420	12	BI506529 BB170027B

ALIGNMENTS

RESULT 1

AY413298

LOCUS AY413298 1743 bp DNA linear GSS 12-DEC-2003

DEFINITION Homo sapiens HCM4844 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY413298

VERSION AY413298.1 GI:39769260

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..1743
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

gene <1..>1743
 /locus_tag="HCM4844"

ORIGIN

Query Match 84.5%; Score 1473; DB 29; Length 1743;

Best Local Similarity 84.5%; Pred. No. 0;

Matches 1473; Conservative 0; Mismatches 270; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Db 61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120

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Qy	181	ACCTGGGTCTGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	NN	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	NN	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	NN	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTCTGCACTGATGGGAGAAATGTTT	420
Db	361	NN	420
Qy	421	TGGGCTGCAGCAATTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	NN	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTGAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTGAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACGTGTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
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Db	781	GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCTTCTTCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTTCTTTGGTCTTGGTGCAGTT	1020

Db	961	 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTCCATGTTTGCA	1080
Db	1021	 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTCCATGTTTGCA	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	 ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAG	1260
Db	1201	 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	 CTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
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Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTAAAA	1440
Db	1381	 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTAAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	 ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
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Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1681	 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Qy	1741	TGA	1743
Db	1741	 TGA	1743

RESULT 2

AY413299

LOCUS AY413299 1743 bp DNA linear GSS 12-DEC-2003

DEFINITION Pan troglodytes HCM4844 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY413299

VERSION AY413299.1 GI:39769261

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

source 1. .1743
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"

gene <1. .>1743
/locus_tag="HCM4844"

ORIGIN

Query Match 83.9%; Score 1463; DB 29; Length 1743;
Best Local Similarity 84.1%; Pred. No. 0;
Matches 1466; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
|||||

Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Db 61 GTTGAATATGGGCTGCCTGGAGAACCACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120

Qy 121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180
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Db 121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACANN 180

Qy 181 ACCTGGGTCTGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240

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Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACGTCAATTCTTAACCAACATTTGCGTCTCCTATCTAGCCAAATAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAAC TTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Db	1621	GAAC TTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAANGGTCTGGGACTGAAGATAATTTACAG	1740
Qy	1741	TGA	1743
Db	1741	TGA	1743

RESULT 3

AK053063

LOCUS AK053063 4097 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930038E20 product:solute carrier family 5 (choline transporter), member 7, full insert sequence.

ACCESSION AK053063

VERSION AK053063.1 GI:26343192
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
 Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4097)
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
 Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4097
/organism="Mus musculus"
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/db_xref="MGI:2424012"
/db_xref="taxon:10090"
/clone="D930038E20"
/tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="15 days embryo"

CDS 512. .2254
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/codon_start=1
/protein_id="BAC35253.1"
/db_xref="GI:26343193"
/translation="MSFHVEGLVAIILFYLLIFLVGIWAAWKTKNSGNPEERSEAIIV
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ORIGIN

Query Match 78.9%; Score 1375; DB 11; Length 4097;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Qy	61	GTGGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
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Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Db	632		691
Qy	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	692		751
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	752		811
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	812		871
Qy	361	ATCTATGGAACCGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC	420
Db	872		931
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	932		991
Qy	481	ATGCACATTTCTGTGCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	992		1051
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTACAGTCTTTTGCATTTTGTAGGGCTGTGG	600
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Qy	601	ATCAGCGTCCCTTTTGCAATTGTACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG	660
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Qy	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG	720
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Qy	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	1232		1291
Qy	781	GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTTCGGG	840
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Qy	841	TGCCTGGTGATGGCCATCCAGCCATACTCATTTGGGGCCATTGGAGCATCAACAGACTGG	900
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Db	1592	CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1651
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Db	1772	CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT	1831
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Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
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Qy	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Db	2132	GAACTTGCACTTGTGAAGCCACGAGAGCCTAACCCTCAGTTCAACTTTCACCAATAAG	2191
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	2192	GAGGCCTTCCTTGATGTTGATTCCAGTCCGAGGGGTCTGGGACTGAAGATAACTTACAA	2251
Qy	1741	TGA	1743

RESULT 4

AK034415

LOCUS AK034415 4306 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330188K24 product:solute carrier family 5 (choline transporter), member 7, full insert sequence.

ACCESSION AK034415

VERSION AK034415.1 GI:26329926

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .4306
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9330188K24"
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CDS 394. .2136
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ORIGIN

[illegible]

Db 1114 CTTGATAATTTTCTGTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG 1173
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 Db 1174 GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTACTGTCCTTCCTGGCAGCTTTTGGG 1233
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 Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
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 Db 1834 ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT 1893
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Qy 1741 TGA 1743
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 Db 2134 TGA 2136

RESULT 5

AY413300

LOCUS AY413300 1743 bp DNA linear GSS 12-DEC-2003

DEFINITION Mus musculus HCM4844 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY413300

VERSION AY413300.1 GI:39769262

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..1743
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ORIGIN

Query Match 66.3%; Score 1156.2; DB 29; Length 1743;
 Best Local Similarity 73.1%; Pred. No. 3.8e-304;
 Matches 1275; Conservative 0; Mismatches 468; Indels 0; Gaps 0;

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 Db 1381 TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA 1440

Qy 1441 ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 || || ||||| ||||| ||||| ||||| || || ||||| |||||
 Db 1441 ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT 1500

Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
 Db 1501 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATGTATTTGATGCTGTTGTGCAAGG 1560

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1561 CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAATATCAAATTAAAT 1620

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 1621 GAACTTGCACTGTGAAACCTCGGCAGAGCCTAACCCCTCAGTTCAACTTTCACCAATAAG 1680

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740

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Db      1681  ||||| |||||||||||||||||||| || |||||||||||||||| |||||
          GAGGCCCTCCTTGATGTTGATTCCAGTCCGAGGGGTCTGGGACTGAAGATAACTTACAA 1740

Qy      1741  TGA 1743
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Db      1741  TGA 1743

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RESULT 6

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AG157499
LOCUS          AG157499                672 bp    DNA    linear    GSS 09-JAN-2002
DEFINITION     Pan troglodytes DNA, clone: RP43-022H02.T7, genomic survey
                sequence.
ACCESSION      AG157499
VERSION        AG157499.1  GI:16687177
KEYWORDS       GSS.
SOURCE         Pan troglodytes (chimpanzee)
  ORGANISM     Pan troglodytes
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1
  AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE        BAC end sequences of Library RPCI-43
  JOURNAL       Unpublished
REFERENCE      2  (bases 1 to 672)
  AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE        Direct Submission
  JOURNAL       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT        Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                end was generated during the R&D process and may have higher chance
                of clone tracking errors.
  PRIMERS
    Sequencing: T7
  LIBRARY
    Vector      : pBACe3.6
    R.Site 1    : EcoRI
    R.Site 2    : EcoRI.
FEATURES
  source        Location/Qualifiers
                1. .672
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="RP43-022H02.T7"
                /sex="male"
                /cell_type="lymphocytes"
                /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN

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Query Match 29.8%; Score 518.8; DB 29; Length 672;
Best Local Similarity 97.3%; Pred. No. 3.5e-130;
Matches 549; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

Qy 1110 AAATGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTGTTGGAGC 1169
 | | ||||||||||||||||||||||||||||||||||||||||
 Db 111 ACAGGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTGTTGGAGC 170

Qy 1170 ATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTC 1229
 ||||||||||||||||||||||||||||||||||||||||
 Db 171 ATCTGCAACAGCCATGGCCTTGCTGACGAAGACTGTGTATGGGCTCTGGTACCTCAGTTC 230

Qy 1230 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 1289
 ||||||||||||||||||||||||||||||||||||||||
 Db 231 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 290

Qy 1290 CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG 1349
 ||||||||||||||||||||||||||||||||||||||||
 Db 291 CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG 350

Qy 1350 GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 1409
 ||||||||||||||||||||||||||||||||||||||||
 Db 351 GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 410

Qy 1410 TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCCTTAAC 1469
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 Db 411 TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACGTCATTCCTTAAC 470

Qy 1470 CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTG-AAAGTGGAACCTTGCCACCTA 1528
 ||||||||| ||||||||||||||| ||||||||| ||||||||||||||||
 Db 471 CAACATTTGCGTCTCCTATCTAGCCAAATATCTATTTGAAAAGTGGAACCTTGCCACCTA 530

Qy 1529 AATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAA 1588
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 Db 531 AATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAA 590

Qy 1589 TTCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGA 1648
 || |||||||||||||||| ||||||||| ||||||||||||||||
 Db 591 TTTTGTCAAAAAATGAAA--TATAAATTAGATGACCTTGCACTTGTGAAGCCACGACAGA 648

Qy 1649 GCATGACCCCTCAGCTCAACTTTCA 1672
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 Db 649 ACATGACCCCTCAGCTTAACTTTCA 672

RESULT 7

CD350164

LOCUS CD350164 707 bp mRNA linear EST 09-JUL-2003

DEFINITION UI-M-FY0-cf1-h-10-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:6851099 5', mRNA sequence.

ACCESSION CD350164

VERSION CD350164.1 GI:31141679

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 707)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 <http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.

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FEATURES
    source
        Location/Qualifiers
            1. .707
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6"
                /db_xref="taxon:10090"
                /clone="IMAGE:6851099"
                /tissue_type="whole brain"
                /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                /lab_host="DH10B (T1 phage resistant)"
                /clone_lib="NIH_BMAP_FY0"
                /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                Site_2: Not I; The library was constructed according
                Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                1996. Denatured RNA was size fractionated on a 1% agarose
                gel. First strand cDNA synthesis was primed with oligo-dT
                primer containing a Not I site. Double strand cDNA was
                size selected according to mRNA size fraction, ligated
                with EcoR I adaptor, digested with NotI and then cloned
                directionally into pYX-Asc vector. The library tag
                sequence located between the Not I site and the polyA tail
                is AGCGAGACAG. This library was created for the University
                Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                Developing Mouse Nervous System', supported by National
                Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                program coordinator."

```

ORIGIN

Query Match 27.1%; Score 472.2; DB 14; Length 707;
Best Local Similarity 86.2%; Pred. No. 1.9e-117;
Matches 580; Conservative 0; Mismatches 88; Indels 5; Gaps 5;

Qy	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Db	27	ATGTCTTTCCACGTAGAAGGACTGGTAGCTATTATCCTCTTCTACCTCCTTATATTTCTG	86
Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	87	GTTGGAATATGGGCTGCATGGAAAACCAAAAACAGCGGCAACCCAGAAGAGCGCAGTGAA	146
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Db	147	GCCATCATAGTCGGGGGCCGTGACATTGGTTTGGTGGTGGTGGTTTACCATGACAGCC	206
Qy	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
 Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
 Kawaji,H., Kawasaki,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
 Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
 Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
 Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G.,
 Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
 Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
 Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
 Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
 Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
 Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
 Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
 Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 22354683
 PUBMED 12466851
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
 Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
 Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
 Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
 Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
 Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
 Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.


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/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

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ORIGIN

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Query Match          23.2%;  Score 404;  DB 10;  Length 516;
Best Local Similarity 86.4%;  Pred. No. 7.2e-99;
Matches 446;  Conservative 0;  Mismatches 70;  Indels 0;  Gaps 0;

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Qy      1067 GTTCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAG 1126
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Db       1   GTTCTATGTTTGTAGAAACATCTAGCAGCTCTCATTAGACAAAACGCTTCGGACAGGG 60

Qy      1127 AAATCGTTTGGGTATGCGAATCACAGTGTGTGTTGGAGCATCTGCAACAGCCATGG 1186
        | ||||| ||||| ||||| ||||||| || ||||||| || ||||||||| |||||
Db       61   AGATCGTCTGGGTATGCGGATCACAGTATTCGTGTTTGGTGCGTCTGCAACAGCCATGG 120

Qy      1187 CCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCG 1246
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Db       121  CCTTGCTGACCAAGACCGTGTATGGGCTCTGGTACCTCAGCTCCGACCTCGTCTACATCA 180

Qy      1247 TTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCG 1306
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Db       181  TTATCTTCCCGCAGCTGCTCTGTGTGCTCTTCATCAAGGGGACCAACACGTACGGGGCCG 240

Qy      1307 TGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATC 1366
        ||||||| || || ||||||| ||||||| |||| || || ||||||| ||| |||
Db       241  TGGCAGGGTACATTGCTGGCCTTTTCCTGAGGGTAACCGGTGGAGAGCCATACCTGAACC 300

Qy      1367 TTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGA 1426
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Db       301  TGCAGCCCTTGATCTTTTACCCTGGTATTACGTTGAAAAAATGGTATATATAATCAGA 360

Qy      1427 AATTTCCATTTAAACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCT 1486
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Db       361  GATTCCCATTTAAACCCCTTGCCATGCTCACCTCCTTCTTATCCAACATTTGCATCTCTT 420

Qy      1487 ATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATG 1546
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Db       421  ATCTAGCCAAATATCTATTTGAAAGTGGAACCTTGCCACCAAATAGATATGTTTGATG 480

Qy      1547 CTGTTGTTGCAAGACACAGTGAAGAAAACATGGATA 1582
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Db       481  CTGTTGTTGCAAGACACAGTGAAGAAAACATGGATA 516

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RESULT 10

BB626260

LOCUS BB626260 650 bp mRNA linear EST 26-OCT-2001

DEFINITION BB626260 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330170D24 5', mRNA sequence.

ACCESSION BB626260

VERSION BB626260.1 GI:16464298
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 650)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
 Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. . 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
 Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
 Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.
 FEATURES Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="9330170D24"

Qy 421 TGGGCTGCAGCAATTT 436
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RESULT 11

AW668962

LOCUS AW668962 541 bp mRNA linear EST 25-APR-2001
DEFINITION 111664 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW668962
VERSION AW668962.1 GI:7525476
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 541)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perteau,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTTCCCAGTCACGACG

Plate: 95 row: L column: 20

Seq primer: ATTTAGGTGACACTATAG.

FEATURES Location/Qualifiers

source 1..541

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 1BOV"

/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN

Query Match 17.9%; Score 312.8; DB 10; Length 541;

Best Local Similarity 85.0%; Pred. No. 5.9e-74;
Matches 350; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Db      130 TCAACAGCCTGGAACCAGACTGCATACGGGCTCTTGCTCCCAGGGAGAAACAGGAGGCA 189

Qy      949 GACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGT 1008
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Db      190 GACATGATCTTGCCGATTGTCCTCAAGTATCTCTGCCCCGTGTACATTTCTTACTTTGGT 249

Qy     1009 CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTCAGCAAGT 1068
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Db      250 CTTGGAGCCGTTTCTGCTGCTGTCATGTCCTCAGCAGATTCTTCCATCTTGTCAGCAAGT 309

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Db      310 TCGATGTTTGCATCGCAACATCTACCAGCTTTCATTTCAGACAAAATGCTTCTGACAAGGAG 369

Qy     1129 ATCGTTTGGGTTATGCGAATCACAGTGTGTTGTGTTTGGAGCATCTGCAACAGCCATGGCC 1188
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      370 ATAGTCTGGGTCATGCGCATCACGGTATTTGTGTTTGGAGCTTCTGCGATGACCATGGCC 429

Qy     1189 TTGCTGACGAAAACACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTTACATCGTT 1248
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Db      430 TTGCTAACGAAGACGGTGTATGGGCTCTGGTACCTCAGCTCTGACCTGGTCTACATCATC 489

Qy     1249 ATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATG 1300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      490 ATCTTCCCGCAGTTGCTCTGCGTGCTCTTCATCAAGGGTACCAACACGTATG 541
```

RESULT 12

BY729567

LOCUS BY729567 675 bp mRNA linear EST 17-DEC-2002

DEFINITION BY729567 RIKEN full-length enriched, 12 days embryo spinal cord Mus musculus cDNA clone C530033E06 5', mRNA sequence.

ACCESSION BY729567

VERSION BY729567.1 GI:27142694

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 675)

AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
 Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
 Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
 Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
 Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
 Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
 Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
 Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
 Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
 Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
 Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
 Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
 Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
 Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
 Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
 Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES Location/Qualifiers

source 1. .675

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="C530033E06"
/tissue_type="spinal cord"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal cord"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
was cleaved with XhoI and BamHI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."

```

ORIGIN

```

Query Match          16.6%;  Score 290;  DB 13;  Length 675;
Best Local Similarity 86.5%;  Pred. No. 1.1e-67;
Matches 320;  Conservative 0;  Mismatches 50;  Indels 0;  Gaps 0;

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Qy      889 TCAACAGACTGGAACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCA 948
      || |||||
Db      306 TCCACAGACTGGAACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCA 365

Qy      949 GACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGT 1008
      |||||
Db      366 GACATGATTTCTCCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGG 425

Qy      1009 CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGT 1068
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Qy      1189 TTGCTGACGAAAACGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTTACATCGTT 1248
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Db      606 TTGCTGACGAAGACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGTGTTTACATCATC 665

Qy      1249 ATCTTCCCCC 1258
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Db      666 ATCTTCCCAC 675

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RESULT 13

BE723927

LOCUS BE723927 524 bp mRNA linear EST 25-APR-2001

DEFINITION 198406 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE723927

VERSION BE723927.1 GI:10125223

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 524)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perteau,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 106 row: L column: 14

Seq primer: ATTTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers

1..524

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 4BOV"

/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN

Query Match 15.7%; Score 274.2; DB 10; Length 524;

Best Local Similarity 84.7%; Pred. No. 2e-63;

Matches 331; Conservative 0; Mismatches 58; Indels 2; Gaps 2;

Qy

889 TCAACAGACTGGAACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCA 948

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Db      130 TCAACATCCTGGAACCACTGCATACGGGCCCTCTTGCTCCCAGGGAGAAACAGGAGGCA 189

Qy      949 GACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGT 1008
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Db      190 GACATGATCTTGCCGATTGTCTCAAGTATCTCTGCCCCGTGTACATTTCTTACTTTGGT 249

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Qy      1247 TTATCTTCCCCCAGCTGCTTTGTGTACTCTT 1277
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      490 TCATCTTCCCGCAGTTGCTCTGCGTGCTCTT 520

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RESULT 14

AL669749

LOCUS AL669749 800 bp mRNA linear EST 14-JAN-2002

DEFINITION AL669749 directional larval cDNA library *Ciona intestinalis* cDNA clone 052ZB03 5', mRNA sequence.

ACCESSION AL669749

VERSION AL669749.1 GI:18143007

KEYWORDS EST.

SOURCE *Ciona intestinalis*

ORGANISM *Ciona intestinalis*

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; *Ciona*.

REFERENCE 1 (bases 1 to 800)

AUTHORS Genoscope.

TITLE *Ciona intestinalis* directional larval cDNA library

JOURNAL Unpublished (2002)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

IMPORTANT: this sequence may contain errors. The *Ciona intestinalis* library from which the clone was isolated may be contaminated with cDNAs from bacteria or other Eukarya.

Directional larval cDNA library originate from Dr.M.Branno, Stazione A.Dohrn, Naples, Italy, and was prepared in pBluescript2SK+.

FEATURES Location/Qualifiers

source 1..800

/organism="Ciona intestinalis"


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Db          651 ATCGTACGGCCTCCCAAGTCCAGTTGANAAAGGCGACCAAGCCAATATTCTACCCATTGT 710
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Db          711 GCTTCAATACCTCACCCCTGTAGCTGTATCATTCTTTGGGGCTTGGCGCTGTTTCTGCT 770
Qy          1027 GCTGTTATGTCATCAGCAGATTCT 1050
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Db          771 GCTGTNATGTCATCTGCCGACTCT 794

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RESULT 15

BW274870
LOCUS BW274870 549 bp mRNA linear EST 11-NOV-2002
DEFINITION BW274870 Nori Satoh unpublished cDNA library, gastrula and neurula
Ciona intestinalis cDNA clone cign070c12 5', mRNA sequence.
ACCESSION BW274870
VERSION BW274870.1 GI:24855481
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 549)
AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

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FEATURES
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                   and neurula"

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ORIGIN

Query Match 13.0%; Score 225.8; DB 13; Length 549;
Best Local Similarity 64.4%; Pred. No. 3.4e-50;
Matches 354; Conservative 0; Mismatches 193; Indels 3; Gaps 1;

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Db      2  ATGTTCTGCTGGTTTAGTGNCTATTATCGTCTTCTACGTTGCTATTCTAGCGATCGGTATTT 61

Qy      71 GGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAAGCCATCATAG 130
        ||  ||  ||||  |  ||  ||  ||  |  |  ||  ||||  |  ||||  |
Db      62 ATGCAGCATGGAGGAAAAGAAGAACCGGAAGAGGAAACGAG---AGCGAGACAATCATGG 118

```

Qy 131 TTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCTACCTGGGTCG 190
 | | | | | | | | | | | | | | | | | | | | | |
 Db 119 TCGGGGGAAGAGACATCGGACTCTTTGTTGGAAGCTTTACTATGACTGCTACGTGGGTAG 178

Qy 191 GAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGTTATGGCCTAGCTT 250
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 Db 179 GTGGTGGTTACATCAACGGCACAGCAGAAGTTGTATACACCCCGGGTTCCGGTCTACTGT 238

Qy 251 GGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTTGCAA 310
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 Db 239 GGACACAAGCGCCATTTGGTTACGGCTGCAGCCTCATGCTTGGCGGGTTGTTTTTCGCTA 298

Qy 311 AACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAAATCTATGGAA 370
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 Db 299 AGAAAATGCGGACTCAGGGTTACGTCACCATGCTGGATCCATTGCAACGTAAGCTTGGCA 358

Qy 371 AACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTCTGGGCTGCAG 430
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 Db 359 GGCATGAGGGGGTCTGTTGTACTTACCAGCACTCTTGGGTGAAATATTCTGGTCAGCCG 418

Qy 431 CAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGATATGCACATTT 490
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 Db 419 CCATCCTTGCCGCTCTTGGCGGTACATTGTCCGTGATCATAGACCTTGATATTCGTATCT 478

Qy 491 CTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATTCTG 550
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 Db 479 CTGTCATTGTATCTGCATGTATTGCTGTGTTGTATACGTTGGTTGGTGGTCTGTATTCGG 538

Qy 551 TGGCCTACAC 560
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 Db 539 TGGCTTATAC 548

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 Job time : 4765 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 09:56:13 ; Search time 6973 Seconds
(without alignments)
10834.205 Million cell updates/sec

Title: US-10-069-541-5
Perfect score: 1743
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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11: gb_sts:*
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14: gb_vi:*
15: em_ba:*
16: em_fun:*
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 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
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 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query					Description
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	4	1743	100.0	1813	9	HSA401466 Homo sapi
	5	1743	100.0	5158	9	AB043997 Homo sapi
	6	1738.2	99.7	1743	6	AR268949 Sequence
	7	1394.2	80.0	1743	6	E49870 High-affini
	8	1394.2	80.0	1743	6	BD012718 High-affi
	9	1394.2	80.0	4904	10	AB030947 Rattus no
	10	1375	78.9	1743	10	AF276872 Mus muscu
	11	1373.4	78.8	1743	6	E49872 High-affini
	12	1373.4	78.8	1743	6	BD012720 High-affi
	13	1373.4	78.8	4938	6	AX080443 Sequence
	14	1367	78.4	1743	10	MMU401467 Mus muscu
	15	867	49.7	2528	5	TMA420808 Torpedo m
	16	730	41.9	1132	5	GGA511267 Gallus ga
	17	630.8	36.2	2239	9	HSA308384 Homo sapi
	18	630.8	36.2	190043	9	AC009963 Homo sapi
	19	502.8	28.8	232792	2	AC106657 Rattus no
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	21	431.4	24.8	3326	3	AY011119 Limulus p
	22	405.8	23.3	3255	3	AY047521 Drosophil
	23	363.8	20.9	1731	6	E49869 High-affini
	24	363.8	20.9	1731	6	BD012717 High-affi
	25	363.8	20.9	1985	3	AB030946 Caenorhab
	26	279.6	16.0	386	6	AX080449 Sequence
	27	242.6	13.9	1461	6	AX432086 Sequence
	28	226	13.0	1657	9	HSA308383 Homo sapi
	29	179.6	10.3	1178	9	HSA308378 Homo sapi
	30	179.6	10.3	186989	3	AC007812 Drosophil
	31	179.6	10.3	189117	3	AC009395 Drosophil
	32	179.6	10.3	255620	3	AE003723 Drosophil
c	33	167.6	9.6	140156	2	AC017381 Drosophil

	34	163	9.4	2326	9	HSA308379	AJ308379 Homo sapi
	35	155	8.9	1467	9	HSA308382	AJ308382 Homo sapi
c	36	151.8	8.7	40893	3	CBRG45E19	AC084631 Caenorhab
	37	150.2	8.6	736	9	HSA308381	AJ308381 Homo sapi
	38	150	8.6	1308	9	HSA308380	AJ308380 Homo sapi
c	39	141.6	8.1	39908	3	CEC48D1	Z81049 Caenorhabdi
c	40	141.6	8.1	330724	2	CEY67H2	AL022475 Caenorhab
c	41	132	7.6	152021	2	AC010923	AC010923 Drosophil
	42	98	5.6	616	11	G84799	G84799 S208P6036FB
c	43	51.8	3.0	10732	6	E32986	E32986 Gene encodi
c	44	49	2.8	2000	6	AX655393	AX655393 Sequence
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ALIGNMENTS

RESULT 1

E49871

LOCUS E49871 1743 bp DNA linear PAT 27-AUG-2002

DEFINITION High-affinity choline transporter.

ACCESSION E49871

VERSION E49871.1 GI:22554902

KEYWORDS JP 2001136976-A/3.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Haga,T. and Okuda,T.

TITLE High-affinity choline transporter

JOURNAL Patent: JP 2001136976-A 3 22-MAY-2001;

SCIENCE & TECH AGENCY

COMMENT OS Homo sapiens (human)

PN JP 2001136976-A/3

PD 22-MAY-2001

PF 27-DEC-1999 JP 1999368991

PI TATSUYA HAGA,TAKASHI OKUDA

PC C12N15/09,A01K67/027,A61K38/00,C07K14/47,C07K16/18,C07K19/00,

PC C12N5/10,

PC C12P21/02,C12P21/08,C12Q1/00,C12N15/00,A61K37/02,C12N5/00 CC

FH Key Location/Qualifiers

FT CDS (1)..(1743).

FEATURES Location/Qualifiers

source 1..1743

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ORIGIN

Query Match 100.0%; Score 1743; DB 6; Length 1743;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60

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Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60

Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
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Db	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Qy	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
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Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC	420
Db	361	ATCTATGGAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC	420
Qy	421	TGGGCTGCAGCAATTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
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Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Qy	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
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Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
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Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
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Qy 1741 TGA 1743

Db 1741 TGA 1743

RESULT 2
BD012719
LOCUS BD012719 1743 bp DNA linear PAT 02-AUG-2002
DEFINITION High-affinity choline transporter.
ACCESSION BD012719
VERSION BD012719.1 GI:22092908
KEYWORDS WO 0116315-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Haga,T. and Okuda,T.
TITLE High-affinity choline transporter
JOURNAL Patent: WO 0116315-A 3 08-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,TATSUYA HAGA,TAKASHI OKUDA
COMMENT OS Homo sapiens (human)
PN WO 0116315-A/3
PD 08-MAR-2001
PF 18-AUG-2000 WO 2000JP005545
PR 27-AUG-1999 JP 99P 240642,27-DEC-1999 JP 99P 368991 PI
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ORIGIN

Query Match 100.0%; Score 1743; DB 6; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60
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Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Qy 181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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 Db 361 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTTC 420
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 Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080
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 Db 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080

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Db	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141	ATGCGAATCACAGTGTGTTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGCGAATCACAGTGTGTTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Db	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Qy	1741	TGA	1743
Db	1741	TGA	1743

RESULT 3

AF276871

LOCUS AF276871 1743 bp mRNA linear PRI 27-NOV-2000

DEFINITION Homo sapiens high affinity choline transporter (SLC5A7) mRNA, complete cds.

ACCESSION AF276871

VERSION AF276871.1 GI:10998441

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Apparsundaram,S., Ferguson,S.M., George,A.L. Jr. and Blakely,R.D.

TITLE Molecular cloning of a human, hemicholinium-3-sensitive choline transporter

JOURNAL Biochem. Biophys. Res. Commun. 276 (3), 862-867 (2000)

MEDLINE 20483599

PUBMED 11027560

REFERENCE 2 (bases 1 to 1743)

AUTHORS Apparsundaram,S., Ferguson,S.M. and Blakely,R.D.

TITLE Direct Submission

JOURNAL Submitted (09-JUN-2000) Department of Pharmacology and Center for Molecular Neuroscience, Vanderbilt University, 23rd Avenue South at Pierce, Nashville, TN 37232-6420, USA

FEATURES Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 1743; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Db	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Db	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Qy	181	ACCTGGGTTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
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Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGTGCGCCTG	300
Db	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGTGCGCCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
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Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTCTGTG	660
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Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
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Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
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Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960

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Db	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
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Db	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGCAAGTTCCATGTTTGCA	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
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Db	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
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Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAACCTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Db	1621	GAACCTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
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Qy	1741	TGA	1743
Db	1741	TGA	1743

RESULT 4
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 DEFINITION Homo sapiens mRNA for high affinity choline transporter (CHT1 gene).
 ACCESSION AJ401466
 VERSION AJ401466.1 GI:9843753
 KEYWORDS CHT1 gene; high affinity choline transporter.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Wieland,A., Bonisch,H. and Bruss,M.
 TITLE Molecular cloning of the human and murine high affinity choline transporters and characterization of the human gene-structure
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1813)
 AUTHORS Bruess,M.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-2000) Bruess M., University of Bonn, Pharmacology and Toxicology, Reuter str. 2b, D-53113 Bonn, GERMANY
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 ORIGIN

Query Match 100.0%; Score 1743; DB 9; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1021		TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCATGTTTGCA	1080
Db	1039		TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCATGTTTGCA	1098
Qy	1081		CGGAACATCTACCAGCTTTCTTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1099		CGGAACATCTACCAGCTTTCTTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1158
Qy	1141		ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
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Db	1219		ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1278
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Db	1339		TCTGGCCTCTTCTTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1398
Qy	1381		TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
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Db	1459		ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1518
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Db 1639 GAACTTGCACCTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1698

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
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Qy 1741 TGA 1743
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Db 1759 TGA 1761

RESULT 5

AB043997

LOCUS AB043997 5158 bp mRNA linear PRI 19-NOV-2000

DEFINITION Homo sapiens mRNA for high-affinity choline transporter CHT1,
 complete cds.

ACCESSION AB043997

VERSION AB043997.1 GI:11231080

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Okuda,T. and Haga,T.

TITLE Functional characterization of the human high-affinity choline
 transporter

JOURNAL FEBS Lett. 484 (2), 92-97 (2000)

MEDLINE 20521663

PUBMED 11068039

REFERENCE 2 (bases 1 to 5158)

AUTHORS Okuda,T.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2000) Takashi Okuda, University of Tokyo, Faculty
 of Medicine, Department of Neurochemistry; 7-3-1 Hongo, Bunkyo-ku,
 Tokyo 1130033, Japan (E-mail:okuda@m.u-tokyo.ac.jp,
 URL:http://park.ecc.u-tokyo.ac.jp/neurochemistry,
 Tel:81-3-5841-3560, Fax:81-3-6814-8154)

FEATURES Location/Qualifiers

source

1. .5158

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CDS

277. .2019

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ORIGIN

Query Match 100.0%; Score 1743; DB 9; Length 5158;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
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Db	1477	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1536
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
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Db	1777	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1836
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Db      2017 TGA 2019

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RESULT 6

AR268949

LOCUS AR268949 1743 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 1 from patent US 6500643.

ACCESSION AR268949

VERSION AR268949.1 GI:29699686

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Wu,D.-H., Gu,Y., Millard,W.J. and He,Y.-J.

TITLE Human high affinity choline transporter

JOURNAL Patent: US 6500643-A 1 31-DEC-2002;

FEATURES Location/Qualifiers

source 1. .1743

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 99.7%; Score 1738.2; DB 6; Length 1743;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1740; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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Db      181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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Qy      241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300

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Db	241	 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
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Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACGTCTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACGTCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCCTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140

Db 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGT 1140
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 Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
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 Db 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
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 Db 1741 TGA 1743

RESULT 7

E49870

LOCUS E49870 1743 bp DNA linear PAT 27-AUG-2002

DEFINITION High-affinity choline transporter.

ACCESSION E49870

VERSION E49870.1 GI:22554901

KEYWORDS JP 2001136976-A/2.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1743)
AUTHORS Haga,T. and Okuda,T.
TITLE High-affinity choline transporter
JOURNAL Patent: JP 2001136976-A 2 22-MAY-2001;
SCIENCE & TECH AGENCY
COMMENT OS Rattus sp. (rat)
PN JP 2001136976-A/2
PD 22-MAY-2001
PF 27-DEC-1999 JP 1999368991
PI TATSUYA HAGA,TAKASHI OKUDA
PC C12N15/09,A01K67/027,A61K38/00,C07K14/47,C07K16/18,C07K19/00,
PC C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/00,C12N15/00,A61K37/02,C12N5/00 CC
FH Key Location/Qualifiers
FT CDS (1)..(1743).

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Matches 1525; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Qy     61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Qy    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT 180
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Qy    181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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Qy    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
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Qy    301 TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360
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Qy    361 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT 420
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Qy    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480
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Db	421	 TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCTACCATCAGCGTAATCATTGATGTGGAT	480
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Db	481	GTGAACATATCGGTCATTGTCTCCGCACTCATTGCCATTCTTTATACCTCGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTACTCTGTGGCATATACTGATGTTGTACAGCTATTCTGCATTTTATAGGATTGTGG	600
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Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATTGAATCAGTTGAAGTCTACACCTGG	720
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Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCTCTACCAGCCATTTGCATTGGGGCCATTGGAGCCTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
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Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
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Qy	1021	TCTGCTGCTGTTATGTCACTCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTCATGTCTCGGCTGACTCATCCATCCTATCAGCAAGTTCCATGTTTGCT	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1140
Qy	1141	ATGCGAATCACAGTGTGTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGAGGATCACTGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTCACGAAG	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGCTCTACATCATCATCTTCCCACAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320

Db 1261 CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1320

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Db 1321 TTTGGACTTTTCCTGAGAATTACCGGAGGAGAGCCATATCTATACTTGCAGCCCTTAATC 1380

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Db 1501 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATATATTTGATGCTGTTGTCTCAAGG 1560

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Db 1621 GAACTTGCACTGTAAAGCCTCGACAGAGCCTAACCTCAGTTCAACTTTCACCAATAAA 1680

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Db 1681 GAGGCTCTCCTTGATGTTGATTCCAGTCCAGAGGGATCTGGGACTGAAGATAACTTACAA 1740

Qy 1741 TGA 1743
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Db 1741 TGA 1743

RESULT 8

BD012718

LOCUS BD012718 1743 bp DNA linear PAT 02-AUG-2002

DEFINITION High-affinity choline transporter.

ACCESSION BD012718

VERSION BD012718.1 GI:22092907

KEYWORDS WO 0116315-A/2.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Haga,T. and Okuda,T.

TITLE High-affinity choline transporter

JOURNAL Patent: WO 0116315-A 2 08-MAR-2001;

JAPAN SCIENCE AND TECHNOLOGY CORP,TATSUYA HAGA,TAKASHI OKUDA

COMMENT OS Rattus norvegicus (rat)

PN WO 0116315-A/2

PD 08-MAR-2001

PF 18-AUG-2000 WO 2000JP005545

PR 27-AUG-1999 JP 99P 240642,27-DEC-1999 JP 99P 368991 PI

TATSUYA HAGA, TAKASHI OKUDA

PC C12N15/12, C07K14/47, C12Q1/68, C07K19/00, C07K16/18, C12N5/10, PC
A61K38/17,

PC A61K45/00, A61P25/28, G01N33/53, A01K67/027

CC

FH Key Location/Qualifiers
FT CDS (1). .(1743).

FEATURES
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Query Match 80.0%; Score 1394.2; DB 6; Length 1743;
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Matches 1525; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Db    481 GTGAACATATCGGTCATTGTCTCCGCACTCATTGCCATTCTTTATACCCTCGTGGGAGGG 540

Qy    541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
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Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG	720
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Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGTTATTACCCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA	1440

Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCCTATCTAGCCAAGTAT	1500
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RESULT 10

AF276872

LOCUS AF276872 1743 bp mRNA linear ROD 28-FEB-2001

DEFINITION Mus musculus sodium and chloride-dependent high-affinity choline transporter mRNA, complete cds.

ACCESSION AF276872

VERSION AF276872.2 GI:13162669

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1743)

AUTHORS Apparsundaram,S., Ferguson,S.M. and Blakely,R.D.

TITLE Molecular cloning and characterization of human and murine high-affinity choline transporters

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1743)

AUTHORS Apparsundaram,S., Ferguson,S.M. and Blakely,R.D.

TITLE Direct Submission

JOURNAL Submitted (09-JUN-2000) Department of Pharmacology and Center for Molecular Neuroscience, Vanderbilt University, 23rd Avenue South at

Pierce, Nashville, TN 37232-6420, USA

REFERENCE 3 (bases 1 to 1743)

AUTHORS Apparsundaram,S., Ferguson,S.M. and Blakely,R.D.

TITLE Direct Submission

JOURNAL Submitted (28-FEB-2001) Department of Pharmacology and Center for Molecular Neuroscience, Vanderbilt University, 23rd Avenue South at Pierce, Nashville, TN 37232-6420, USA

REMARK Sequence update by submitter

COMMENT On Feb 28, 2001 this sequence version replaced gi:11527247.

FEATURES

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ORIGIN

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ORIGIN

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Best Local Similarity 86.7%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

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Db      1741 TGA 1743

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RESULT 13

AX080443

LOCUS AX080443 4938 bp DNA linear PAT 22-FEB-2001

DEFINITION Sequence 1 from Patent WO0078950.

ACCESSION AX080443

VERSION AX080443.1 GI:13159872

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Sierzega,M. and Albrandt,K.

TITLE Differentially expressed genes in the adipocytes of obese mice

JOURNAL Patent: WO 0078950-A 1 28-DEC-2000;

AMYLIN PHARMACEUTICALS, INC. (US)

FEATURES

Location/Qualifiers

source

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ORIGIN

Query Match 78.8%; Score 1373.4; DB 6; Length 4938;

Best Local Similarity 86.7%; Pred. No. 0;

Matches 1512; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

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Qy      121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180

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Db 1927 GAGGCCCTCCTTGATGTTGATTCCAGTCCGAGGGGTCTGGGACTGAAGATAACTTACAA 1986

Qy 1741 TGA 1743
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Db 1987 TGA 1989

LOCUS MMU401467 1743 bp mRNA linear ROD 16-AUG-2000
 DEFINITION Mus musculus mRNA for high affinity choline transporter (CHT1 gene).
 ACCESSION AJ401467
 VERSION AJ401467.1 GI:9843808
 KEYWORDS ChT1 gene; high affinity choline transporter.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Wieland,A., Bonisch,H. and Bruss,M.
 TITLE Molecular cloning of the human and murine high affinity choline transporters and characterization of the human gene-structure
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1743)
 AUTHORS Bruess,M.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-2000) Bruess M., University of Bonn, Pharmacology and Toxicology, Reuter str. 2b, D-53113 Bonn, GERMANY

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 CDS 1. .1743
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 Best Local Similarity 86.5%; Pred. No. 0;
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Qy 1741 TGA 1743

111

Db 1741 TGA 1743

RESULT 15

TMA420808

LOCUS TMA420808 2528 bp mRNA linear VRT 27-NOV-2001

DEFINITION Torpedo marmorata mRNA for high affinity choline transporter (CHT1 gene).

ACCESSION AJ420808

VERSION AJ420808.1 GI:17148508

KEYWORDS CHT1 gene; high affinity choline transporter.

SOURCE Torpedo marmorata (marbled electric ray)

ORGANISM Torpedo marmorata

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.

REFERENCE 1

AUTHORS Guermonprez, L., O'Regan, S., Meunier, F.M. and Morot-Gaudry-Talarmain, Y.

TITLE Cyclosporin, FK506 and rapamycin inhibit neuronal choline uptake via calcineurin-dependent and independent mechanisms

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2528)

AUTHORS O'Regan, S.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2001) O'Regan S., Neurobiologie Cellulaire et Moleculaire, C.N.R.S., 1 av de la Terrasse, F-91198 Gif-sur-Yvette, FRANCE

FEATURES Location/Qualifiers

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CDS 49..1803
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AATSMALLAQSIYGLWYLSSDLVYVIIFPQLISVLFVKGTNTYGSIAGYIIGFLLRIS
GGEPYLHMQPFIYYPGCYLDHSFGDDPVYVQRFPFKTMAMLFSLGNTGVSYLKYLEF
VSGILPPKLDLDSVSVKHSKEIMDKTFLMNQDNITLSELVHVNPISASVSAALTNK
EAFEDIEPNPELSKSGND"

polyA_signal 2487. .2492
/gene="CHT1"

ORIGIN

Query Match 49.7%; Score 867; DB 5; Length 2528;
Best Local Similarity 69.3%; Pred. No. 2.9e-227;
Matches 1217; Conservative 0; Mismatches 520; Indels 18; Gaps 2;

```
Qy      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
      ||| | | || | || || | |||| ||| || |||| ||| | |||| || |
Db      49 ATGACCGTTCACATCGATGGGATCGTAGCGATCGTCCTGTTTACTTGTTAATCTTATTT 108

Qy      61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCA-----GCGCAGAAGAGCGC 114
      ||||| ||||| |||| ||| ||||| | | ||| || ||
Db      109 GTTGGATTATGGGCTGCTTGGAAAAGTAAAAACACGTCAATGGAAGGAGCAATGGATCGG 168

Qy      115 AGCGAAGCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATG 174
      || ||||| || || |||| || ||||| || | ||||| || || |||
Db      169 AGTGAAGCTATAATGATTGGGGGAAGAGATATCGGGCTGCTGTTGGTGGCTTCACAATG 228

Qy      175 ACAGCTACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCA 234
      || || || ||||| || || ||||| |||| || || ||||| ||
Db      229 ACCGCAACTTGGGTCGGTGGCGGTTATATCAATGGGACAGCAGAGGCGGTTTATGTTCT 288

Qy      235 GGTTATGGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGT 294
      || || ||| | || |||| |||| || | |||| | || || ||| || ||
Db      289 GGTACGGCTTGGCCTGGGCGCAGGCTCCCTTCGGATACGCACTCAGCCTGGTTATTGGC 348

Qy      295 GGCCTGTTCTTTGCAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTT 354
      ||| | || || || |||| |||| || | ||| || ||||| || |||||
Db      349 GGCTTATTTTTCGCTAAACCCATGCGCTCACGGGGTTACGTGACCATGCTGGACCCGTTT 408

Qy      355 CAGCAAATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTCTGCACTGATGGGAGAA 414
      || || || || |||| |||| || | || || || || || || || ||
Db      409 CAACAGATGTACGGTAAACGAATGGGAGGATTGCTCTTCATCCCGCTCTCTGGGGGAA 468

Qy      415 ATGTTCTGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGAT 474
      || ||||| ||||| || | || || | || || | ||||| || ||
Db      469 ATCTTCTGGTCTGCAGCCATACTGTCCGCGCTAGGTGCAACTTTAAGCGTGATTGTGGAC 528

Qy      475 GTGGATATGCACATTTCTGTTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTG 534
      | |||| || || || || | || || | || || | |||| |||||
Db      529 ATCAATATAAACGTATCAGTGGTAGTTTCCGCTGTGATCGCTGTATTATACACTCTGGTC 588

Qy      535 GGAGGGCTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGG 594
      || ||| | || || || |||| ||||| ||| | ||||| || ||||
Db      589 GGCGGGTTATACTCGGTCGCGTACACAGATGTCGTCCAGTTGTTTGCATCTTCTTAGGT 648

Qy      595 CTGTGGATCAGCGTCCCCCTTTCGATTGTACATCCTGCAGTCGCAGACATCGGGTTCACT 654
      ||||| |||| || || || || || || || || || || || || ||
Db      649 TTGTGGATCAGCATCCCTTTCGCCCTCTTAAATCCCGCTGTTACGGATATTATCGTGACC 708
```

Qy 655 GCTGTGCATGCCAAATACCAAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTAC 714
 || || | || | ||| ||| ||||| | | | ||| || |
 Db 709 GCAAATCAAGAAGTTTATCAGGAGCCTTGGGTGGGAAATATACAATCAAAGGACAGTTTA 768

Qy 715 TCTTGGCTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTT 774
 ||| |||| | |||| | ||||| ||||| ||||| ||| |||
 Db 769 ATCTGGATTGACAACTTTCTATTACTGATGCTGGGTGGAATCCCGTGGCAAGTATATTTT 828

Qy 775 CAGAGGGTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCT 834
 ||||| || || ||| ||| || || ||||| ||||| ||||| ||||| ||
 Db 829 CAGAGAGTCCTTTCTGCTTCTTCTGCTACCTATGCGCAAGTCCTGTCCTTTCTGGCTGCC 888

Qy 835 TTCGGGTGCCTGGTGATGGCCATCCAGCCATACTCATTGGGGCCATTGGAGCATCAACA 894
 ||||| ||| | | ||||| ||| | ||||| || || || ||| ||| ||
 Db 889 TTCGGTTGCGTTCTCATGGCCATCCCGTCTGTTCTCATCGGTGCAATAGGAACATCCACT 948

Qy 895 GACTGGAACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATG 954
 ||||| ||||| | ||||| | |||| || | | | ||| | | |||
 Db 949 GACTGGAATCAGACTTCCTATGGCTTGCCAGGCCCTATAGGCAAAAATGAGACTGATATG 1008

Qy 955 ATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGT 1014
 ||||| || || || ||||| |||| || || || ||||| || ||||| |||||
 Db 1009 ATTTTGCCGATCGTGCTGCAGCATCTGTGTCCACCCTACATTTCTTTTGGTCTTGGC 1068

Qy 1015 GCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTCAGCAAGTTCCATG 1074
 || || ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||
 Db 1069 GCTGTCTCTGCTGCTGTGATGTCATCGGCTGATTCTTCTATCTTATCAGCAAGTTCTATG 1128

Qy 1075 TTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTT 1134
 ||||| ||||| || ||||| ||| | ||||| || ||||| ||||| ||||| ||
 Db 1129 TTTGCTCGGAATATTTACCATCTTGCTTTCAGACAAGAGGCTTCAGACAAAGAAATAGTG 1188

Qy 1135 TGGGTTATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTG 1194
 ||||| ||||| ||||| | ||| | ||||| | ||||| ||||| ||||| |||||
 Db 1189 TGGGTAATGCGAATCACCATATTTCTATTTGGAGGAGCTGCAACATCTATGGCATTGCTT 1248

Qy 1195 ACGAAAACCTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTC 1254
 | || | | |||| ||||| || || || || ||||| ||| || ||||| ||
 Db 1249 GCTCAATCAATCTATGGCCTCTGGTATCTGAGCTCAGATCTTGTCTACGTCAATTATCTTT 1308

Qy 1255 CCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGT 1314
 || || | | | || |||| || ||||| ||||| ||||| | | || ||
 Db 1309 CCTCAATTAATATCAGTGCTCTTCGTCAAGGGAACAAACACATATGGGTCTATTGCTGGA 1368

Qy 1315 TATGTTTCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCC 1374
 ||| | |||| | || || || || || || ||||| | || | |||||
 Db 1369 TATATCATTGGCTTTTTGCTTCGGATTAGTGGTGGTGAACCATATTTACATATGCAGCCA 1428

Qy 1375 TTGATCTTCTACCCTGGCT-----ATTACCCTGATGATAATGGTATATATAAT 1422
 || || | ||||| || ||| | || || || || || || ||
 Db 1429 TTTATTTATTACCCTGGATGCTATTTAGATCATTCCTTTGGAGATGATCCTGTTTATGTT 1488

Qy 1423 CAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCCTTAACCAACATTTGCATC 1482
 |||| ||||| ||||| || || || || || |||| ||||| ||| |
 Db 1489 CAGAGATTTCCCTTTAAACCATGGCAATGTTATTCTCCTTCTTGGGCAACACTGGTGTA 1548

Qy	1483	TCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTT	1542
Db	1549	TCATATCTTGTCAAGTACCTGTTTCGTAAGTGGAATATTGCCACCAAATTAGACTTCCTT	1608
Qy	1543	GATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAAT	1602
Db	1609	GACAGCGTTGTATCAAAACACAGTAAGGAAATCATGGACAAAACATTCTTGATGAATCAG	1668
Qy	1603	GAAAATATTAAATTAGATGAACTTGCACCTGTGAAGCCACGACAGAGCATGACCCTCAGC	1662
Db	1669	GACAATATTACTTTGTCAGAGCTGGTGCATGTTAATCCAATACACAGTGCTTCAGTTAGT	1728
Qy	1663	TCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGG	1722
Db	1729	GCTGCTTTGACCAATAAGGAAGCATTTGAAGACATTGAGCCAAATCCTGAACTTTCTAAG	1788
Qy	1723	ACTGAAGATAATTTA	1737
Db	1789	TCAGGCAATGATTGA	1803

Search completed: March 22, 2004, 13:57:28
Job time : 6988 secs

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 09:53:04 ; Search time 742 Seconds
 (without alignments)
 9979.258 Million cell updates/sec

Title: US-10-069-541-5
 Perfect score: 1743
 Sequence: 1 atggcctttccatgtggaagg.....ctgaagataatttacagtga 1743

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1743	100.0	1743	4	AAF81712	Aaf81712 Human hig
2	1743	100.0	1743	5	AAH49207	Aah49207 Human CHO
3	1743	100.0	1743	9	ADD50638	Add50638 cDNA enco
4	1743	100.0	1813	9	ADD50646	Add50646 High-affi
5	1738.2	99.7	1743	8	ABX94338	Abx94338 Human cDN
6	1394.2	80.0	1743	4	AAF81711	Aaf81711 Rat high
7	1394.2	80.0	4904	9	ADD50642	Add50642 cDNA enco

	8	1375	78.9	1743	9	ADD50640	Add50640 cDNA enco
	9	1375	78.9	1743	9	ADD50660	Add50660 cDNA enco
	10	1373.4	78.8	1743	4	AAF81713	Aaf81713 Mouse hig
	11	1373.4	78.8	4938	5	AAD02457	Aad02457 Mouse P4P
	12	630.8	36.2	8760	5	AAH49206	Aah49206 Human CHO
	13	630.8	36.2	119040	9	ADD50656	Add50656 BAC seque
	14	630.8	36.2	142299	9	ADD50651	Add50651 BAC seque
	15	363.8	20.9	1731	4	AAF81710	Aaf81710 C. elegan
	16	363.8	20.9	1985	9	ADD50644	Add50644 High-affi
	17	279.6	16.0	386	5	AAD02461	Aad02461 Mouse P4P
	18	266.6	15.3	1729	4	ABL29569	Abl29569 Drosophil
	19	242.6	13.9	1461	6	ABK73210	Abk73210 Bacillus
	20	180.8	10.4	10140	5	AAH49201	Aah49201 Human CHO
c	21	180.8	10.4	119040	9	ADD50656	Add50656 BAC seque
c	22	180.8	10.4	142299	9	ADD50651	Add50651 BAC seque
c	23	179.6	10.3	4223	4	ABL29568	Abl29568 Drosophil
	24	167.6	9.6	1094	5	AAS82193	Aas82193 DNA encod
	25	163	9.4	240	5	AAH49203	Aah49203 Human CHO
	26	155	8.9	455	4	AAI11913	Aai11913 Probe #18
	27	155	8.9	455	4	ABA53620	Aba53620 Human foe
	28	155	8.9	455	4	AAI33245	Aai33245 Probe #19
	29	155	8.9	455	4	ABA23372	Aba23372 Probe #18
	30	155	8.9	455	4	AAK27341	Aak27341 Human bon
	31	155	8.9	455	4	AAK01883	Aak01883 Human bra
	32	155	8.9	455	4	ABS26913	Abs26913 Human liv
	33	155	8.9	455	5	AAI01851	Aai01851 Probe #18
	34	154.6	8.9	300	5	AAH49204	Aah49204 Human CHO
	35	150.8	8.7	240	5	AAH49205	Aah49205 Human CHO
	36	108	6.2	180	5	AAH49202	Aah49202 Human CHO
	37	72	4.1	96	4	AAI21121	Aai21121 Probe #11
	38	72	4.1	96	4	ABA66205	Aba66205 Human foe
	39	72	4.1	96	4	AAI46388	Aai46388 Probe #15
	40	72	4.1	96	4	ABA33269	Aba33269 Probe #11
	41	72	4.1	96	4	AAK40366	Aak40366 Human bon
	42	72	4.1	96	4	AAK14621	Aak14621 Human bra
	43	72	4.1	96	4	ABS39934	Abs39934 Human liv
	44	72	4.1	96	5	AAI06841	Aai06841 Probe #68
	45	60	3.4	60	6	ABN37501	Abn37501 Human spl

ALIGNMENTS

RESULT 1

AAF81712

ID AAF81712 standard; cDNA; 1743 BP.

XX

AC AAF81712;

XX

DT 01-JUN-2001 (first entry)

XX

DE Human high affinity choline transporter protein encoding cDNA.

XX

KW High affinity choline transporter; cho-1; Alzheimer's disease; diagnosis;
KW ss.

XX

OS Homo sapiens.

Db	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTTCACATCCTGCAGTCGCAGACATCGGGTTCCTGCTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTTCACATCCTGCAGTCGCAGACATCGGGTTCCTGCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTTCTTTGGTCTTGGTGCAGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080

Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Db	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA	1680
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Qy	1741	TGA	1743
Db	1741	TGA	1743

RESULT 2

AAH49207

ID AAH49207 standard; cDNA; 1743 BP.

XX

AC AAH49207;

XX

DT 26-NOV-2001 (first entry)

XX
DE Human CHOT encoding cDNA.
XX
KW CHOT; human; choline transporter; chromosome 2q11-13; nootropic;
KW neuroprotective; gene therapy; antisense therapy; degenerative disease;
KW cognitive disorder; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX
PN DE10009055-A1.
XX
PD 30-AUG-2001.
XX
PF 28-FEB-2000; 2000DE-01009055.
XX
PR 28-FEB-2000; 2000DE-01009055.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
DR WPI; 2001-590709/67.
DR P-PSDB; AAB86837.
XX
PT A new gene encoding human choline transporter, designated hCHOT is
PT located on chromosome 2q11-13 and is useful to treat degenerative
PT disorders such as Alzheimer's disease.
XX
PS Disclosure; Page 11; 12pp; German.
XX
CC This invention describes a novel gene encoding human choline transporter,
CC designated hCHOT which is located on chromosome 2q11-13. The products of
CC the invention have nootropic and neuroprotective activity and can be used
CC for gene or antisense therapy. (I) is used to treat degenerative disease,
CC particularly cognitive disorders such as Alzheimer's disease. Sense and
CC antisense oligonucleotides derived from the gene may be used in
CC diagnostics and other techniques. This sequence encodes the human CHOT
CC protein described in the invention
XX
SQ Sequence 1743 BP; 412 A; 393 C; 406 G; 532 T; 0 U; 0 Other;

Query Match 100.0%; Score 1743; DB 5; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCTTTCATGTGGAAGGACTGATAGCTATCATCGTGTTCCTACCTTCTAATTTTGCTG	60
Db	1	ATGGCTTTCATGTGGAAGGACTGATAGCTATCATCGTGTTCCTACCTTCTAATTTTGCTG	60
Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	61	GTTGGAATATGGGCTGCCTGGAGAACCACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Db	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180

Qy	181	ACCTGGGTCTGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	ACCTGGGTCTGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTGAGTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTGAGTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGG	840
Db	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCAGCCATACTCATGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCCATCCAGCCATACTCATGGGGCCATTGGAGCATCAACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTCTTTGGTCTTGGTGCAGTT	1020

Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGTCAGCAAGTTCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGTCAGCAAGTTCATGTTTGCA	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGT	1140
Db	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGT	1140
Qy	1141	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACATCATTTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Qy	1621	GAACTTGCACTTGTTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA	1680
Db	1621	GAACTTGCACTTGTTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA	1680
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Qy	1741	TGA	1743
Db	1741	TGA	1743

RESULT 3

ADD50638

ID ADD50638 standard; cDNA; 1743 BP.

XX

AC ADD50638;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE cDNA encoding human high-affinity choline transporter (hCHT).
 XX
 KW Human; high-affinity choline transporter; hCHT; chromosome 2q12;
 KW cholinergic function; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; schizophrenia; dysautonomia; myasthenia gravis;
 KW brain; cholinergic signalling; antiparkinsonian; anticonvulsant;
 KW nootropic; neuroprotective; neuroleptic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .1743
 FT /*tag= a
 FT /product= "hCHT"
 XX
 PN US2003114399-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 23-JUL-2001; 2001US-00911077.
 XX
 PR 23-JUL-2001; 2001US-00911077.
 XX
 PA (BLAK/) BLAKELY R D.
 PA (APPA/) APPARSUNDARAM S.
 PA (FERG/) FERGUSON S.
 XX
 PI Blakely RD, Apparsundaram S, Ferguson S;
 XX
 DR WPI; 2003-810914/76.
 DR P-PSDB; ADD50639.
 XX
 PT Novel isolated polynucleotide encoding human or mouse high affinity
 PT choline transporter polypeptide, useful in gene therapy to increase
 PT cholinergic function in a cell of a patient suffering from Alzheimer's
 PT disease.
 XX
 PS Claim 2; SEQ ID NO 1; 74pp; English.
 XX
 CC The present invention relates to the isolation of polynucleotide
 CC sequences encoding human and mouse high-affinity choline transporter
 CC (hCHT and mCHT respectively), and the proteins they encode. The gene
 CC encoding hCHT is located on chromosome 2q12. The polynucleotide sequence
 CC encoding hCHT, is useful for expressing hCHT recombinantly. The hCHT
 CC polynucleotide sequence when delivered to a cell, increases cholinergic
 CC function in the cell that is in a patient having Parkinson's disease,
 CC Huntington's disease, Alzheimer's disease, schizophrenia, dysautonomia or
 CC myasthenia gravis. The hCHT antibody is useful for controlling
 CC transporter CHT proteins to the brain, and for treating the above
 CC mentioned diseases. The antibody is also useful for diagnosing the above
 CC mentioned disorders and to detect the influence of cholinergic
 CC signalling. The present sequence encodes hCHT. Note: The sequence data
 CC for this patent was obtained in electronic format directly from the USPTO

CC web site at seqdata.uspto.gov.

XX

SQ Sequence 1743 BP; 412 A; 393 C; 406 G; 532 T; 0 U; 0 Other;

Query Match 100.0%; Score 1743; DB 9; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60
      |||
Db      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60

Qy     61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
      |||
Db     61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120

Qy    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT 180
      |||
Db    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT 180

Qy    181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
      |||
Db    181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240

Qy    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
      |||
Db    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300

Qy    301 TTCTTTGCAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360
      |||
Db    301 TTCTTTGCAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360

Qy    361 ATCTATGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC 420
      |||
Db    361 ATCTATGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC 420

Qy    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480
      |||
Db    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480

Qy    481 ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG 540
      |||
Db    481 ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG 540

Qy    541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
      |||
Db    541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600

Qy    601 ATCAGCGTCCCCTTTGCATTGTACACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG 660
      |||
Db    601 ATCAGCGTCCCCTTTGCATTGTACACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG 660

Qy    661 CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG 720
      |||
Db    661 CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG 720

Qy    721 CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG 780
```

Db	721		CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781		GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	781		GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Qy	841		TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841		TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Qy	901		AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901		AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961		CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTGGTCTTGGTGCAGTT	1020
Db	961		CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTGGTCTTGGTGCAGTT	1020
Qy	1021		TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021		TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Qy	1081		CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081		CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141		ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141		ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201		ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201		ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261		CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261		CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321		TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321		TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381		TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381		TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441		ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441		ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501		CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501		CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Qy	1561		CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620

Db 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA 1680
 |||

Db 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA 1680

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 |||

Db 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740

Qy 1741 TGA 1743
 |||

Db 1741 TGA 1743

RESULT 4

ADD50646

ID ADD50646 standard; DNA; 1813 BP.

XX

AC ADD50646;

XX

DT 15-JAN-2004 (first entry)

XX

DE High-affinity choline transporter (CHT) associated DNA sequence #2.

XX

KW High-affinity choline transporter; CHT; cholinergic function;
 KW Parkinson's disease; Huntington's disease; Alzheimer's disease;
 KW schizophrenia; dysautonomia; myasthenia gravis; brain;
 KW cholinergic signalling; antiparkinsonian; anticonvulsant; nootropic;
 KW neuroprotective; neuroleptic; ds.

XX

OS Unidentified.

XX

PN US2003114399-A1.

XX

PD 19-JUN-2003.

XX

PF 23-JUL-2001; 2001US-00911077.

XX

PR 23-JUL-2001; 2001US-00911077.

XX

PA (BLAK/) BLAKELY R D.

PA (APPA/) APPARSUNDARAM S.

PA (FERG/) FERGUSON S.

XX

PI Blakely RD, Apparsundaram S, Ferguson S;

XX

DR WPI; 2003-810914/76.

XX

PT Novel isolated polynucleotide encoding human or mouse high affinity
 PT choline transporter polypeptide, useful in gene therapy to increase
 PT cholinergic function in a cell of a patient suffering from Alzheimer's
 PT disease.

XX

PS Disclosure; SEQ ID NO 9; 74pp; English.

XX

CC The present invention relates to the isolation of polynucleotide

CC sequences encoding human and mouse high-affinity choline transporter
CC (hCHT and mCHT respectively), and the proteins they encode. The gene
CC encoding hCHT is located on chromosome 2q12. The polynucleotide sequence
CC encoding hCHT, is useful for expressing hCHT recombinantly. The hCHT
CC polynucleotide sequence when delivered to a cell, increases cholinergic
CC function in the cell that is in a patient having Parkinson's disease,
CC Huntington's disease, Alzheimer's disease, schizophrenia, dysautonomia or
CC myasthenia gravis. The hCHT antibody is useful for controlling
CC transporter CHT proteins to the brain, and for treating the above
CC mentioned diseases. The antibody is also useful for diagnosing the above
CC mentioned disorders and to detect the influence of cholinergic
CC signalling. The present DNA sequence of unknown function is provided in
CC the electronic sequence data but is not mentioned in the printed
CC specification. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at seqdata.uspto.gov.
XX
SQ Sequence 1813 BP; 440 A; 406 C; 417 G; 550 T; 0 U; 0 Other;

Query Match 100.0%; Score 1743; DB 9; Length 1813;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Db	19	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	78
Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	79	GTTGGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	138
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Db	139	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	198
Qy	181	ACCTGGGTTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	199	ACCTGGGTTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	258
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	259	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	318
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	319	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	378
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Db	379	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	438
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	439	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	498
Qy	481	ATGCACATTTCTGTGCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	499	ATGCACATTTCTGTGCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	558

Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	559	CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG	618
Qy	601	ATCAGCGTCCCCCTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG	660
Db	619	ATCAGCGTCCCCCTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG	678
Qy	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	679	CATGCCAAATACCAAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	738
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	739	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	798
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	799	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	858
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	859	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	918
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	919	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	978
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	979	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1038
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTCCATGTTTGCA	1080
Db	1039	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTCCATGTTTGCA	1098
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1099	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1158
Qy	1141	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1159	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1218
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1219	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1278
Qy	1261	CTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1279	CTGCTTTGTGTACTCTTTGTAAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1338
Qy	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1339	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1398

Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 |||
 Db 1399 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1458

Qy 1441 ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 |||
 Db 1459 ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1518

Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 |||
 Db 1519 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1578

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 |||
 Db 1579 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1638

Qy 1621 GAACCTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA 1680
 |||
 Db 1639 GAACCTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA 1698

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 |||
 Db 1699 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1758

Qy 1741 TGA 1743
 |||
 Db 1759 TGA 1761

RESULT 5

ABX94338

ID ABX94338 standard; cDNA; 1743 BP.

XX

AC ABX94338;

XX

DT 13-JUN-2003 (first entry)

XX

DE Human cDNA encoding high affinity choline transporter, HACT.

XX

KW Human; ss; gene; HACT; high affinity choline transporter; pain;
 KW neurotransmitter biosynthesis; learning and memory; aging; epilepsy;
 KW neurological disorder; spasticity; myoclonus; muscle spasm;
 KW muscle hyperactivity; stroke; head trauma; neuronal cell death;
 KW multiple sclerosis; spinal chord injury; dystonia; Alzheimer's disease;
 KW Myasthenia Gravis; multi-infarct dementia; AIDS dementia;
 KW Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
 KW ALS; attention deficit disorder; organic brain syndrome; schizophrenia;
 KW nicotine addiction; memory disorder; cognitive disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .1743

FT /*tag= a

FT /product= "HACT"

XX

PN US6500643-B1.

XX
 PD 31-DEC-2002.
 XX
 PF 07-SEP-2000; 2000US-00657252.
 XX
 PR 07-SEP-2000; 2000US-00657252.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Wu D, Gu Y, Millard WJ, He Y;
 XX
 DR WPI; 2003-361535/34.
 DR P-PSDB; ABU08979.
 XX
 PT Novel isolated polynucleotide (I) that encodes high affinity choline
 PT transporter protein, useful for preventing, treating or ameliorating
 PT neurological and cognitive disorders such as Alzheimer's or Parkinson's
 PT disease.
 XX
 PS Claim 2; Col 17-21; 20pp; English.
 XX
 CC The invention relates to an isolated polynucleotide which encodes a high
 CC affinity choline transporter (HACT) protein appearing as ABU08979. Also
 CC included are a polynucleotide encoding a fragment consisting of at least
 CC about 50 amino acids of the HACT protein, a vector comprising the
 CC polynucleotide, a composition comprising a vector comprising a
 CC polynucleotide which comprises at least about 12 contiguous nucleic acids
 CC of a polynucleotide appearing as ABX94339 (encoding choline
 CC acetyltransferase), a recombinant host cell which comprises the vector
 CC (used to express the HACT protein or fragment). The polynucleotide is
 CC useful as a probe or primer to detect the presence of HACT polynucleotide
 CC in a sample, such as a biological sample, or for screening for test
 CC agents which bind to the polynucleotide. A pharmaceutical composition
 CC comprising the polynucleotide is useful for preventing, treating or
 CC ameliorating neurological and cognitive disorders e.g. pain, spasticity,
 CC myoclonus, muscle spasm, muscle hyperactivity, epilepsy, stroke, head
 CC trauma, neuronal cell death, multiple sclerosis, spinal chord injury,
 CC dystonia, Alzheimer's disease, myasthenia gravis, multi- infarct
 CC dementia, AIDS dementia, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis (ALS), attention deficit disorder, nicotine
 CC addiction, organic brain syndromes, schizophrenia or memory and cognitive
 CC disorders. HACT is thought to be the rate limiting step in cholinergic
 CC neurotransmitter biosynthesis and regeneration (cholinergic transmissions
 CC are crucial to brain functions such as learning and memory). The present
 CC sequence encodes human HACT
 XX
 SQ Sequence 1743 BP; 411 A; 395 C; 405 G; 532 T; 0 U; 0 Other;

Query Match 99.7%; Score 1738.2; DB 8; Length 1743;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1740; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGCTG 60
 Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120

Db	61	 GTTGGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Db	121	 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT	180
Qy	181	ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	 TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTTC	420
Db	361	 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTTC	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	 ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTACGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	 CTCTATTCTGTGGCCTACACTGATGTCGTTACGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	 ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	 CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTAGAGG	780
Db	721	 CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTAGAGG	780
Qy	781	GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGG	840
Db	781	 GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCCTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960

Db 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
 Qy 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
 Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080
 Qy 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
 Qy 1141 ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1141 ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
 Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
 Qy 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 Qy 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
 Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 Qy 1441 AACTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1441 AACTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTTACCAATAAA 1680
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTTACCAATAAA 1680
 Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAA 1740
 Qy 1741 TGA 1743
 |||
 Db 1741 TGA 1743

RESULT 6

AAF81711

ID AAF81711 standard; cDNA; 1743 BP.

XX

AC AAF81711;

XX

DT 01-JUN-2001 (first entry)

XX

DE Rat high affinity choline transporter protein encoding cDNA.

XX

KW High affinity choline transporter; cho-1; Alzheimer's disease; diagnosis;
KW ss.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 1. .1743

FT /*tag= a

FT /product= "high affinity choline transporter"

XX

PN WO200116315-A1.

XX

PD 08-MAR-2001.

XX

PF 18-AUG-2000; 2000WO-JP005545.

XX

PR 27-AUG-1999; 99JP-00240642.

PR 27-DEC-1999; 99JP-00368991.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

PI Haga T, Okuda T;

XX

DR WPI; 2001-226688/23.

DR P-PSDB; AAB74664.

XX

PT New rat and human spinal cord high affinity choline transporters, useful
PT in diagnosis of Alzheimer's disease and screening promoters as drugs for
PT treating Alzheimer's disease.

XX

PS Claim 6; Page 64-68; 90pp; Japanese.

XX

CC The present sequence encodes a rat (Rattus norvegicus) high affinity
CC choline transporter protein designated cho-1. The cho-1 protein has
CC nootropic and neuroprotective activities. The cho-1 polynucleotide and
CC protein can be used for the diagnosis of diseases related to the
CC expression of cho-1 by comparing the cho-1 polynucleotide sequence in a
CC sample to that of a control. Drug compositions containing the cho-1
CC protein or expression promoters or inhibitors of cho-1 are useful for
CC treating disorders characterised by abnormal levels of cho-1, such as
CC Alzheimer's disease

XX

SQ Sequence 1743 BP; 414 A; 402 C; 404 G; 523 T; 0 U; 0 Other;

Query Match

80.0%; Score 1394.2; DB 4; Length 1743;

Best Local Similarity 87.5%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Qy      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
      ||| ||||| ||||| ||||| ||| || ||| ||||| ||||| || || |||
Db      1 ATGCCTTTCCATGTAGAAGGACTAGTAGCGATTATCCTGTTCTACCTTCTTATATTTCTG 60

Qy     61 GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
      ||||| ||||| ||||| ||||| ||||| ||| || ||||| ||||| |||||
Db     61 GTTGGAATATGGGCTGCATGGAAAACCAAAAACAGCGGTAATGCAGAAGAACGCAGCGAA 120

Qy    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 GCCATCATAGTTGGGGGCCGAGACATTGGTTTGTGGTTGGTGGTGGTTTACCATGACAGCC 180

Qy    181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
      ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Db    181 ACCTGGGTTGGAGGAGGTTACATCAACGGGACAGCTGAAGCAGTTTATGGGCCAGGTTGT 240

Qy    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 GGTCTAGCTTGGGCTCAGGCACCCATTGGATATTCTCTGAGTCTGATTTTAGGTGGCCTG 300

Qy    301 TTCTTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 TTTTTTGCAAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCGTTTCAACAG 360

Qy    361 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTTC 420
      ||||| ||||| || || ||||| || ||||| ||||| ||||| |||||
Db    361 ATCTATGGAAAGCGCATGGGTGGGCTGCTGTTTCATCCCTGCACTGATGGGAGAGATGTTTC 420

Qy    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480
      ||||| ||||| ||||| || || || ||||| ||||| ||||| |||||
Db    421 TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCTACCATCAGCGTAATCATTGATGTGGAT 480

Qy    481 ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG 540
      || |||| || |||| |||| ||||| ||||| || || || |||||
Db    481 GTGAACATATCGGTCATTGTCTCCGCACTCATTGCCATTCTTTATACCCTCGTGGGAGGG 540

Qy    541 CTCTATTCTGTGGCTTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
      |||| ||||| || ||||| || ||||| || ||||| |||| |||||
Db    541 CTCTACTCTGTGGCATATACTGATGTTGTACAGCTATTCTGCATTTTATAGGATTGTGG 600

Qy    601 ATCAGCGTCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAC TGCTGTG 660
      |||| |||| |||| ||||| ||||| ||||| ||||| ||||| |||||
Db    601 ATCAGTGTCCATTTGCCCTGTCACATCCTGCAGTCACCGACATTGGATTCAC TGCTGTG 660

Qy    661 CATGCCAAATACCAAAAGCCGTGGCTGGGAAC TGTGACTCATCTGAAGTCTACTCTTGG 720
      |||| ||||| || || ||||| |||| |||| ||||| ||||| |||||
Db    661 CATGCTAAATACAGAGTCCCTGGCTGGGAACCAT TGAATCAGTTGAAGTCTACACCTGG 720

Qy    721 CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 CTTGATAATTTTCTGTTGTTGATGCTGGGTGGAATACCATGGCAAGCCTACTTCCAGAGG 780

Qy    781 GTTCTCTCTTCTTCTCCTCAGCCACCTATGCTCAAGTGCTGTCTTCTTCTGGCAGCTTTCGGG 840
      || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db	781	GTCCCTCTCTTCATCGTCAGCGACCTATGCTCAGGTGCTGTCCCTTCCTGGCAGCTTTTGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCTCTACCAGCCATTTCGATTGGGGCCATTGGAGCCTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAAACTGCATATGGGTTTCCAGATCCCAAGACCAAGGAGGAAGCAGACATGATTCTC	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTGGTCTTGGTGCAGTT	1020
Db	961	CCGATTGTTCTACAGTACCTCTGCCCTGTGTACATTTCTTTCTTTGGGCTTGGTGTCTGTT	1020
Qy	1021	TCTGCTGCTGTTATGTTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTCATGTCCTCGGCTGACTCATCCATCCTATCAGCAAGTTCCATGTTTGCT	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1140
Qy	1141	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGAGGATCACTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTCACGAAG	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGCTCTACATCATCATCTTCCCACAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT	1320
Qy	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TTTGGACTTTTCTCTGAGAATTACCGGAGGAGAGCCATATCTATACTTGACGCCCTTAATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGTTATTACCCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACTCTCTCCATGGTTACCTCATTCCTTACCAACATTTGTGTTTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCCTCAAATTTAGATATATTTGATGCTGTTGTCTCAAGG	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAATGAAAATATTAAATTAGAT	1620
Db	1561	CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAACATCAAATTAAAT	1620
Qy	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAAA	1680
Db	1621	GAACTTGCACTTGTGAAGCCACGACAGAGCCTAACCCCTCAGTTCAACTTTCACCAATAAAA	1680

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 ||||| ||||||||||||||||||||||||| || ||||||||||||||||||| |||||
 Db 1681 GAGGCTCTCCTTGATGTTGATTCCAGTCCAGAGGGATCTGGGACTGAAGATAACTTACAA 1740

Qy 1741 TGA 1743
 |||
 Db 1741 TGA 1743

RESULT 7
 ADD50642

ID ADD50642 standard; cDNA; 4904 BP.

XX

AC ADD50642;

XX

DT 15-JAN-2004 (first entry)

XX

DE cDNA encoding rat high-affinity choline transporter (rCHT).

XX

KW Rat; high-affinity choline transporter; rCHT; cholinergic function;

KW Parkinson's disease; Huntington's disease; Alzheimer's disease;

KW schizophrenia; dysautonomia; myasthenia gravis; brain;

KW cholinergic signalling; antiparkinsonian; anticonvulsant; nootropic;

KW neuroprotective; neuroleptic; gene; ss.

XX

OS Rattus sp.

XX

FH	Key	Location/Qualifiers
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FT	CDS	224. .1966
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FT		/*tag= a
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FT		/product= "rCHT"
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XX

PN US2003114399-A1.

XX

PD 19-JUN-2003.

XX

PF 23-JUL-2001; 2001US-00911077.

XX

PR 23-JUL-2001; 2001US-00911077.

XX

PA (BLAK/) BLAKELY R D.

PA (APPA/) APPARSUNDARAM S.

PA (FERG/) FERGUSON S.

XX

PI Blakely RD, Apparsundaram S, Ferguson S;

XX

DR WPI; 2003-810914/76.

DR P-PSDB; ADD50643.

XX

PT Novel isolated polynucleotide encoding human or mouse high affinity

PT choline transporter polypeptide, useful in gene therapy to increase

PT cholinergic function in a cell of a patient suffering from Alzheimer's

PT disease.

XX

PS Example 1; SEQ ID NO 5; 74pp; English.

XX

Qy 541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
 ||||| ||||| || ||||| || ||||| || ||||| ||||| |||||
 Db 764 CTCTACTCTGTGGCATATACTGATGTTGTACAGCTATTCTGCATTTTATAGGATTGTGG 823

Qy 601 ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 824 ATCAGTGTCCCATTTGCCCTGTCACATCCTGCAGTCACCGACATTGGATTCACTGTGTG 883

Qy 661 CATGCCAAATACCAAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG 720
 ||||| ||||| || || ||||| ||||| ||||| || || ||||| ||||| |||||
 Db 884 CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATGAATCAGTTGAAGTCTACACCTGG 943

Qy 721 CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG 780
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 944 CTTGATAATTTTCTGTTGTTGATGCTGGGTGGAATACCATGGCAAGCCTACTTCCAGAGG 1003

Qy 781 GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG 840
 || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1004 GTCCTCTCTTCATCGTCAGCGACCTATGCTCAGGTGCTGTCCTTCCTGGCAGCTTTTGGG 1063

Qy 841 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG 900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1064 TGCCTGGTGATGGCTCTACCAGCCATTTGCATTGGGGCCATTGGAGCCTCCACAGACTGG 1123

Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1124 AACCAAACTGCATATGGGTTTCCAGATCCCAAGACCAAGGAGGAAGCAGACATGATTCTC 1183

Qy 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1184 CCGATTGTTCTACAGTACCTCTGCCCTGTGTACATTTCTTCTTTGGGCTTGGTGTCTGTT 1243

Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGCAAGTTCCATGTTTGCA 1080
 ||||| ||||| ||||| || || || || || ||||| || ||||| ||||| |||||
 Db 1244 TCTGCTGCTGTCATGTCTCGGCTGACTCATCCATCCTATCAGCAAGTTCCATGTTTGCT 1303

Qy 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1304 CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATGTGTGGGTC 1363

Qy 1141 ATGCGAATCACAGTGTGTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
 ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1364 ATGAGGATCACTGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTCACGAAG 1423

Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
 ||||| ||||| ||||| || ||||| ||||| ||||| || ||||| ||||| |||||
 Db 1424 ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGCTTACATCATCATCTTCCCACAG 1483

Qy 1261 CTGCTTTGTGTAATCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 ||||| ||||| ||||| || || ||||| ||||| ||||| || || ||||| |||||
 Db 1484 CTGCTCTGTGTAATCTTCAACGAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1543

Qy 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
 | ||| || ||||| ||||| || ||||| ||||| || || ||||| |||||
 Db 1544 TTTGGACTTTTCTGAGAATTACCGGAGGAGAGCCATATCTATACTTGACGCCCTTAATC 1603

Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1604	TTCTACCCTGGTTATTACCCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA	1663
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1664	ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCCTATCTAGCCAAGTAT	1723
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1724	CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATATATTTGATGCTGTTGTCTCAAGG	1783
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620
Db	1784	CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAACATCAAATTAAAT	1843
Qy	1621	GAACTTGCACCTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTACCAATAAA	1680
Db	1844	GAACTTGCACCTGTAAAGCCTCGACAGAGCCTAACCTCAGTTCAACTTTACCAATAAA	1903
Qy	1681	GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG	1740
Db	1904	GAGGCTCTCCTTGATGTTGATTCCAGTCCAGAGGGATCTGGGACTGAAGATAACTTACAA	1963
Qy	1741	TGA	1743
Db	1964	TGA	1966

ADD50640

XX

XX

XX

XX

KW

KW

KW

OS

FH

FT

FT

XX

XX

XX

XX
PR 23-JUL-2001; 2001US-00911077.
XX
PA (BLAK/) BLAKELY R D.
PA (APPA/) APPARSUNDARAM S.
PA (FERG/) FERGUSON S.
XX
PI Blakely RD, Apparsundaram S, Ferguson S;
XX
DR WPI; 2003-810914/76.
DR P-PSDB; ADD50641.
XX
PT Novel isolated polynucleotide encoding human or mouse high affinity
PT choline transporter polypeptide, useful in gene therapy to increase
PT cholinergic function in a cell of a patient suffering from Alzheimer's
PT disease.
XX
PS Claim 30; SEQ ID NO 3; 74pp; English.
XX
CC The present invention relates to the isolation of polynucleotide
CC sequences encoding human and mouse high-affinity choline transporter
CC (hCHT and mCHT respectively), and the proteins they encode. The gene
CC encoding hCHT is located on chromosome 2q12. The polynucleotide sequence
CC encoding hCHT, is useful for expressing hCHT recombinantly. The hCHT
CC polynucleotide sequence when delivered to a cell, increases cholinergic
CC function in the cell that is in a patient having Parkinson's disease,
CC Huntington's disease, Alzheimer's disease, schizophrenia, dysautonomia or
CC myasthenia gravis. The hCHT antibody is useful for controlling
CC transporter CHT proteins to the brain, and for treating the above
CC mentioned diseases. The antibody is also useful for diagnosing the above
CC mentioned disorders and to detect the influence of cholinergic
CC signalling. The present sequence encodes mCHT. Note: The sequence data
CC for this patent was obtained in electronic format directly from the USPTO
CC web site at seqdata.uspto.gov.
XX
SQ Sequence 1743 BP; 406 A; 409 C; 410 G; 518 T; 0 U; 0 Other;

Query Match 78.9%; Score 1375; DB 9; Length 1743;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Db	1	ATGCCTTTCCATGTGGAAGGACTGGTAGCTATTATCCTCTTCTACCTCCTTATATTTCTG	60
QY	61	GTTGGAATATGGGCTGCCTGGAGAACCACAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	61	GTTGGAATATGGGCTGCATGGAACAAAACAGCGGCAACCCAGAAGAGCGCAGTGAA	120
QY	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Db	121	GCCATCATAGTCGGGGGCCGTGACATTGTTTGTGGTTGGTGGTGGTTTACCATGACAGCC	180
QY	181	ACCTGGGTTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	ACCTGGGTTGGAGGAGGCTACATCAATGGGACAGCAGAAGCAGTGTATGGGCCAGGTTGT	240

Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGTCTAGCTTGGGCTCATGCACCCATTGGATATTCTCTGAGTCTAATTTTAGGTGGTCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTTTTTGCGAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCATTCAAACAG	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAGCGCATGGGTGGGCTGCTCTTCATCCCTGCACTGATGGGAGAGATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCCACCATCAGCGTGATCATTGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	GTGAACATATCGGTCATTGTCTCTGCACTCATTGCCATTCTTTATACCCTAGTGGGTGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTTGTAGGGCTGTGG	600
Db	541	CTCTACTCTGTGGCATATACTGATGTTGTCCAGCTATTCTGCATTTTTATAGGACTGTGG	600
Qy	601	ATCAGCGTCCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	ATCAGTGTCCCTTTTGGCCTGTCTACATCCTGCAGTCACCGACATCGGATTCACAGCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATGAATCAGTTGAAGTCTACACCTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTTCAGAGG	780
Db	721	CTTGATAATTTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTTCGGG	840
Db	781	GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTACTGTCCTTCCTGGCAGCTTTTGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATTCTC	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGTCTGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCTATCAGCAGATTCTTCCATCTTGTCTAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCAGCTGCTGTCATGTCCTCAGCTGACTCGTCCATCCTGTCGGCGAGTTCTATGTTTGCT	1080
Qy	1081	CGGAACATCTACCAGCTTTTCTTCAGACAAAATGCTTCGGACAAAAGAAATCGTTTGGGTT	1140

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Db      1081 CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC 1140
Qy      1141 ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
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Db      1141 ATGAGGATCACTGTGCTTGTGTTTCGGAGCATCTGCAACAGCCATGGCTTTGCTGACGAAG 1200
Qy      1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1201 ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGTCTACATCATCATCTTCCCACAG 1260
Qy      1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
      ||||| ||||| ||||| | || ||||| ||||| ||||| || || ||||| ||
Db      1261 CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1320
Qy      1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
      | ||| || ||||| ||||| ||||| ||||| ||||| || || ||||| |||
Db      1321 TTTGGACTATTCTGAGAATTACTGGAGGAGAGCCATATCTATACTGCAGCCCTTAATC 1380
Qy      1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
      ||||| ||||| ||||| ||||| | ||||| ||||| ||||| || ||||| ||
Db      1381 TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA 1440
Qy      1441 ACACTTGCCATGGTTACATCATTCCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
      || || ||||| ||||| ||||| ||||| ||||| | || ||||| |||||
Db      1441 ACTCTCTCCATGGTTACCTCATTCCTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT 1500
Qy      1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1501 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATGTATTTGATGCTGTTGTCGCAAGG 1560
Qy      1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      1561 CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAATATCAAATTAAAT 1620
Qy      1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
      ||||| ||||| ||||| || || ||||| | ||||| ||||| ||||| |||||
Db      1621 GAACTTGCACTGTGAAACCTCGGCAGAGCCTAACCCTCAGTTCAACTTTCACCAATAAG 1680
Qy      1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1681 GAGGCCCTCCTTGATGTTGATTCCAGTCCGAGGGGTCTGGGACTGAAGATAATTTACAA 1740
Qy      1741 TGA 1743
      |||
Db      1741 TGA 1743

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RESULT 9

ADD50660

ID ADD50660 standard; cDNA; 1743 BP.

XX

AC ADD50660;

XX

DT 15-JAN-2004 (first entry)

XX

DE cDNA encoding mouse high-affinity choline transporter (mCHT) #2.

XX
 KW Mouse; high-affinity choline transporter; mCHT; cholinergic function;
 KW Parkinson's disease; Huntington's disease; Alzheimer's disease;
 KW schizophrenia; dysautonomia; myasthenia gravis; brain;
 KW cholinergic signalling; antiparkinsonian; anticonvulsant; nootropic;
 KW neuroprotective; neuroleptic; gene; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .1743
 FT /*tag= a
 FT /product= "mCHT #2"
 XX
 PN US2003114399-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 23-JUL-2001; 2001US-00911077.
 XX
 PR 23-JUL-2001; 2001US-00911077.
 XX
 PA (BLAK/) BLAKELY R D.
 PA (APPA/) APPARSUNDARAM S.
 PA (FERG/) FERGUSON S.
 XX
 PI Blakely RD, Apparsundaram S, Ferguson S;
 XX
 DR WPI; 2003-810914/76.
 DR P-PSDB; ADD50661.
 XX
 PT Novel isolated polynucleotide encoding human or mouse high affinity
 PT choline transporter polypeptide, useful in gene therapy to increase
 PT cholinergic function in a cell of a patient suffering from Alzheimer's
 PT disease.
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 PS Example 4; SEQ ID NO 23; 74pp; English.
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 CC The present invention relates to the isolation of polynucleotide
 CC sequences encoding human and mouse high-affinity choline transporter
 CC (hCHT and mCHT respectively), and the proteins they encode. The gene
 CC encoding hCHT is located on chromosome 2q12. The polynucleotide sequence
 CC encoding hCHT, is useful for expressing hCHT recombinantly. The hCHT
 CC polynucleotide sequence when delivered to a cell, increases cholinergic
 CC function in the cell that is in a patient having Parkinson's disease,
 CC Huntington's disease, Alzheimer's disease, schizophrenia, dysautonomia or
 CC myasthenia gravis. The hCHT antibody is useful for controlling
 CC transporter CHT proteins to the brain, and for treating the above
 CC mentioned diseases. The antibody is also useful for diagnosing the above
 CC mentioned disorders and to detect the influence of cholinergic
 CC signalling. The present sequence encodes mCHT. Note: The sequence data
 CC for this patent was obtained in electronic format directly from the USPTO
 CC web site at seqdata.uspto.gov.
 XX
 SQ Sequence 1743 BP; 406 A; 409 C; 410 G; 518 T; 0 U; 0 Other;

Query Match 78.9%; Score 1375; DB 9; Length 1743;

Best Local Similarity 86.8%; Pred. No. 0;
Matches 1513; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

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Qy      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Db      1 ATGCCTTTCCATGTGGAAGGACTGGTAGCTATTATCCTCTTCTACCTCCTTATATTTCTG 60

Qy     61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
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Db     61 GTTGAATATGGGCTGCATGGAAAACCAAAACAGCGGCAACCCAGAAGAGCGCAGTGAA 120

Qy    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180
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Db    121 GCCATCATAGTCGGGGGCCGTGACATTGGTTTGTGGTTGGTGGTTTTACCATGACAGCC 180

Qy    181 ACCTGGGTGCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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Db    181 ACCTGGGTGGGAGGAGGCTACATCAATGGGACAGCAGAAGCAGTGTATGGGCCAGGTTGT 240

Qy    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
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Db    241 GGTCTAGCTTGGGCTCATGCACCCATTGGATATTCTCTGAGTCTAATTTTAGGTGGTCTG 300

Qy    301 TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360
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Db    301 TTTTTCGCAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCATTCAAACAG 360

Qy    361 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCCTGCACTGATGGGAGAAATGTTTC 420
      ||||| ||||| || || || || || || ||||| ||||| ||||| |||||
Db    361 ATCTATGGAAAGCGCATGGGTGGGCTGCTCTTCATCCCTGCACTGATGGGAGAGATGTTTC 420

Qy    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480
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Qy    481 ATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG 540
      || |||| || ||||| ||||| ||||| ||||| || || || || |||| |||
Db    481 GTGAACATATCGGTCAATTGTCTCTGCACTCATTGCCATTCTTTATACCCTAGTGGGTGGG 540

Qy    541 CTCTATTCTGTGGCCTACACTGATGTGCTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
      ||||| ||||| || ||||| || ||||| || ||||| ||||| ||||| |||||
Db    541 CTCTACTCTGTGGCATATACTGATGTTGTCCAGCTATTCTGCATTTTATAGGACTGTGG 600

Qy    601 ATCAGCGTCCCCTTTGCATTGTCTACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG 660
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Db    601 ATCAGTGTCCCTTTTGGCCTGTCTACATCCTGCAGTCACCGACATCGGATTACAGCTGTG 660

Qy    661 CATGCCAAATACCAAAAGCCGTGGCTGGGAACGTGTTGACTCATCTGAAGTCTACTCTTGG 720
      ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db    661 CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATGAATCAGTTGAAGTCTACACCTGG 720

Qy    721 CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    721 CTTGATAAATTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG 780

Qy    781 GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG 840
      || ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||
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Db 781 GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTACTGTCCTTCCTGGCAGCTTTTGGG 840

Qy 841 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG 900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 841 TGCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG 900

Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
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Db 901 AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATTCTC 960

Qy 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
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Db 961 CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGTCTGTT 1020

Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGCAAGTTCCATGTTTGCA 1080
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Db 1021 TCAGCTGCTGTGTCCTCAGCTGACTCGTCCATCCTGTGCGCGAGTTCTATGTTTGCT 1080

Qy 1081 CGGAACATCTACCAGCTTTCTTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
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Db 1081 CGGAATATCTACCAGCTTTCTTTCAGACAAAATGCATCAGACAAGGAAATGTGTGGGTC 1140

Qy 1141 ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
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Db 1141 ATGAGGATCACTGTGCTTGTGTTTCGGAGCATCTGCAACAGCCATGGCTTGCTGACGAAG 1200

Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
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Db 1201 ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGCTTACATCATCTTCCCACAG 1260

Qy 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
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Db 1261 CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1320

Qy 1321 TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
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Db 1321 TTTGGACTATTCTCTGAGAATTACTGGAGGAGAGCCATATCTATACTTGAGCCCTTAATC 1380

Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1381 TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTAAA 1440

Qy 1441 AACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 || || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1441 ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT 1500

Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
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Db 1501 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATGTATTTGATGCTGTTGTCGCAAGG 1560

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1561 CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAATATCAAATTAAAT 1620

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1621 GAACTTGCACTGTGAAACCTCGGCAGAGCCTAACCCTCAGTTCAACTTTCACCAATAAG 1680

CC control. Drug compositions containing the cho-1 protein or expression
CC promoters or inhibitors of cho-1 are useful for treating disorders
CC characterised by abnormal levels of cho-1, such as Alzheimer's disease
XX
SQ Sequence 1743 BP; 407 A; 410 C; 409 G; 517 T; 0 U; 0 Other;

Query Match 78.8%; Score 1373.4; DB 4; Length 1743;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1512; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

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Qy      1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Db      1 ATGTCTTTCCACGTAGAAAGGACTGGTAGCTATTATCCTCTTCTACCTCCTTATATTCTG 60

Qy     61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 GTTGAATATGGGCTGCATGGAACCAAAACAGCGGCAACCCAGAAGAGCACAGTGAA 120

Qy    121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180
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Db    121 GCCATCATAGTCGGGGCCGTGACATTGGTTTGTGGTTGGTGGTTTACCATGACAGCC 180

Qy    181 ACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT 240
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Db    181 ACCTGGGTTGGAGGAGGCTACATCAATGGGACAGCAGAAGCAGTGTATGGGCCAGGTTGT 240

Qy    241 GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG 300
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Db    241 GGTCTAGCTTGGGCTCAGGCACCCATTGGATATTCTCTGAGTCTAATTTTAGGTGGTCTG 300

Qy    301 TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA 360
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Db    301 TTTTGTGCGAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCATTTCACAG 360

Qy    361 ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCTCTGCACTGATGGGAGAAATGTTT 420
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Db    361 ATCTATGGAAAGCGCATGGGTGGGCTGCTCTTCATCCCTGCACTGATGGGAGAGATGTTT 420

Qy    421 TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT 480
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Db    421 TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCCACCATCAGCGTGATCATTGATGTGGAT 480

Qy    481 ATGCACATTTCTGTTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG 540
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Db    481 GTGAACATATCGGTCATTGTCTCTGCACTCATTGCCATTCTTTATACCCTAGTGGGTGGG 540

Qy    541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG 600
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Db    541 CTCTACTCTGTGGCATATACTGATGTTGTCCAGCTATTCTGCATTTTATAGGACTGTGG 600

Qy    601 ATCAGCGTCCCCTTTGCATTGTACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG 660
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Db    601 ATCAGTGTCCCTTTGCCCTGTACATCCTGCAGTCACCGACATCGGATTACAGCTGTG 660

Qy    661 CATGCCAAATACCAAAAGCCGTGGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG 720
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Qy	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAATTTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG	780
Qy	781	GTTCTCTCTTCTTCTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGG	840
Db	781	GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTAAGTGCTGTCCTTCTGGCAGCTTTTGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATCTC	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGCCTTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGCAAGTTCATGTTTGCA	1080
Db	1021	TCAGCTGCTGTCATGTCCTCAGCTGACTCGTCCATCTGTGCGCGAGTTCTATGTTTGCT	1080
Qy	1081	CGGAACATCTACCAGCTTTCTTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAATATCTACCAGCTTTCTTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1140
Qy	1141	ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGAGGATCACTGTGCTTGTGTTTCGGAGCATCTGCAACAGCCATGGCTTTGCTGACGAAG	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTACATCGTTATCTTCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGTCTACATCATCATCTTCCCACAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT	1320
Qy	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TTTGGACTATTTCTGAGAATTACTGGAGGAGAGCCATATCTATACTTGAGCCCTTAATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCCTCAAATTAGATGTATTTGATGCTGTTGTCGCAAGG	1560

Db 727 GTGAACATATCGGTCATTGTCTCTGCACTCATTGCCATTCTTTATACCCTAGTGGGTGGG 786
 Qy 541 CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG 600
 Db 787 CTCTACTCTGTGGCATATACTGATGTTGTCCAGCTATTCTGCATTTTATAGGACTGTGG 846
 Qy 601 ATCAGCGTCCCCTTTGCATTGTACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG 660
 Db 847 ATCAGTGTCCCTTTTGCCCTGTACATCCTGCAGTCACCGACATCGGATTACAGCTGTG 906
 Qy 661 CATGCCAAATACCAAAAGCCGTGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG 720
 Db 907 CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATTGAATCAGTTGAAGTCTACACCTGG 966
 Qy 721 CTTGATAGTTTCTGTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG 780
 Db 967 CTTGATAATTTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG 1026
 Qy 781 GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGTCTTCCTTCCCTGGCAGCTTTCGGG 840
 Db 1027 GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTACTGTCCTTCCCTGGCAGCTTTCGGG 1086
 Qy 841 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG 900
 Db 1087 TGCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG 1146
 Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
 Db 1147 AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATTCCTC 1206
 Qy 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
 Db 1207 CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGTCTGTT 1266
 Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080
 Db 1267 TCAGCTGCTGTCATGTCCTCAGCTGACTCGTCCATCCTGTGCGCGAGTTCTATGTTTGCT 1326
 Qy 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
 Db 1327 CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC 1386
 Qy 1141 ATGCGAATCACAGTGTTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
 Db 1387 ATGAGGATCACTGTGCTTGTGTTGCGAGCATCTGCAACAGCCATGGCTTTGCTGACGAAG 1446
 Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAG 1260
 Db 1447 ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGCTTACATCATCATCTTCCCACAG 1506
 Qy 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 Db 1507 CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1566
 Qy 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380

Db 1567 TTTGGACTATTCTTGAGAATTACTGGAGGAGAGCCATATCTATACTTGCAGCCCTTAATC 1626

Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTAAAA 1440
 ||||| ||||| ||||| | ||||| ||||| || |||||

Db 1627 TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA 1686

Qy 1441 AACTTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 || || ||||| ||||| ||||| ||||| ||||| |||||

Db 1687 ACTCTCTCCATGGTTACCTCATCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT 1746

Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
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Db 1747 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATGTATTTGATGCTGTTGTCGCAAGG 1806

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAATATTAAATTAGAT 1620
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1807 CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAATATCAAATTAAAT 1866

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 ||||| ||||| || || ||||| | ||||| ||||| |||||

Db 1867 GAACTTGCACTGTGAAACCTCGGCAGAGCCTAACCTCAGTTCAACTTTCACCAATAAG 1926

Qy 1681 GAGGCCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 ||||| ||||| ||||| ||||| || || ||||| ||||| |||||

Db 1927 GAGGCCCTCCTTGATGTTGATTCCAGTCCGGAGGGTCTGGGACTGAAGATAACTTACAA 1986

Qy 1741 TGA 1743
 |||

Db 1987 TGA 1989

RESULT 12

AAH49206

ID AAH49206 standard; DNA; 8760 BP.

XX

AC AAH49206;

XX

DT 26-NOV-2001 (first entry)

XX

DE Human CHOT exons 6, 7, 8 and 3' UTR region DNA.

XX

KW CHOT; human; choline transporter; chromosome 2q11-13; nootropic;

KW neuroprotective; gene therapy; antisense therapy; degenerative disease;

KW cognitive disorder; Alzheimer's disease; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .4853

FT /*tag= a

FT /product= "CHOT"

FT /note= "This sequence is interrupted by introns"

FT exon 41. .194

FT /*tag= b

FT /number= 6

FT intron 195. .2456

FT /*tag= c

FT /number= 6
 FT exon 2455. .2674
 FT /*tag= d
 FT /number= 7
 FT intron 2675. .4223
 FT /*tag= e
 FT /number= 7
 FT exon 4224. .4853
 FT /*tag= f
 FT /number= 8
 FT 3'UTR 4854. .8760
 FT /*tag= g

XX

PN DE10009055-A1.

XX

PD 30-AUG-2001.

XX

PF 28-FEB-2000; 2000DE-01009055.

XX

PR 28-FEB-2000; 2000DE-01009055.

XX

PA (BRUE/) BRUESS M.

PA (BOEN/) BOENISCH H.

XX

PI Bruess M, Boenisch H;

XX

DR WPI; 2001-590709/67.

XX

PT A new gene encoding human choline transporter, designated hCHOT is
 PT located on chromosome 2q11-13 and is useful to treat degenerative
 PT disorders such as Alzheimer's disease.

XX

PS Disclosure; Page 9-11; 12pp; German.

XX

CC This invention describes a novel gene encoding human choline transporter,
 CC designated hCHOT which is located on chromosome 2q11-13. The products of
 CC the invention have nootropic and neuroprotective activity and can be used
 CC for gene or antisense therapy. (I) is used to treat degenerative disease,
 CC particularly cognitive disorders such as Alzheimer's disease. Sense and
 CC antisense oligonucleotides derived from the gene may be used in
 CC diagnostics and other techniques. This sequence represents exons 6-8 and
 CC the 3' UTR fragment encoding the human CHOT protein described in the
 CC invention

XX

SQ Sequence 8760 BP; 2727 A; 1619 C; 1565 G; 2849 T; 0 U; 0 Other;

Query Match 36.2%; Score 630.8; DB 5; Length 8760;
 Best Local Similarity 99.7%; Pred. No. 1.8e-172;
 Matches 632; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1110 AAATGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTTTGTGTTTGGAGC 1169
 | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4220 ACAGGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTTTGTGTTTGGAGC 4279
 Qy 1170 ATCTGCAACAGCCATGGCCTTGCTGACGAAAACGTGTATGGGCTCTGGTACCTCAGTTC 1229
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4280 ATCTGCAACAGCCATGGCCTTGCTGACGAAAACGTGTATGGGCTCTGGTACCTCAGTTC 4339

Qy	1230	TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC	1289
Db	4340	TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC	4399
Qy	1290	CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG	1349
Db	4400	CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG	4459
Qy	1350	GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA	1409
Db	4460	GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA	4519
Qy	1410	TGGTATATATAATCAGAAATTTCCATTTAAAACACTTGCCATGGTTACATCATTTCTTAAC	1469
Db	4520	TGGTATATATAATCAGAAATTTCCATTTAAAACACTTGCCATGGTTACATCATTTCTTAAC	4579
Qy	1470	CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA	1529
Db	4580	CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA	4639
Qy	1530	ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT	1589
Db	4640	ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT	4699
Qy	1590	TCTTGTCAAAAATGAAAATATTAAATTAGATGAACCTTGCACTTGTGAAGCCACGACAGAG	1649
Db	4700	TCTTGTCAAAAATGAAAATATTAAATTAGATGAACCTTGCACTTGTGAAGCCACGACAGAG	4759
Qy	1650	CATGACCCTCAGCTCAACTTTTACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC	1709
Db	4760	CATGACCCTCAGCTCAACTTTTACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC	4819
Qy	1710	AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA	1743
Db	4820	AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA	4853

RESULT 13

ADD50656

ID ADD50656 standard; DNA; 119040 BP.

XX

AC ADD50656;

XX

DT 15-JAN-2004 (first entry)

XX

DE BAC sequence containing hCHT gene.

XX

KW Human; high-affinity choline transporter; hCHT; chromosome 2q12;

KW cholinergic function; Parkinson's disease; Huntington's disease;

KW Alzheimer's disease; schizophrenia; dysautonomia; myasthenia gravis;

KW brain; cholinergic signalling; antiparkinsonian; anticonvulsant;

KW nootropic; neuroprotective; neuroleptic; bacterial artificial chromosome;

KW BAC; ds.

XX

OS Homo sapiens.

XX

PN US2003114399-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 23-JUL-2001; 2001US-00911077.
 XX
 PR 23-JUL-2001; 2001US-00911077.
 XX
 PA (BLAK/) BLAKELY R D.
 PA (APPA/) APPARSUNDARAM S.
 PA (FERG/) FERGUSON S.
 XX
 PI Blakely RD, Apparsundaram S, Ferguson S;
 XX
 DR WPI; 2003-810914/76.
 XX
 PT Novel isolated polynucleotide encoding human or mouse high affinity
 PT choline transporter polypeptide, useful in gene therapy to increase
 PT cholinergic function in a cell of a patient suffering from Alzheimer's
 PT disease.
 XX
 PS Example 3; SEQ ID NO 19; 74pp; English.
 XX
 CC The present invention relates to the isolation of polynucleotide
 CC sequences encoding human and mouse high-affinity choline transporter
 CC (hCHT and mCHT respectively), and the proteins they encode. The gene
 CC encoding hCHT is located on chromosome 2q12. The polynucleotide sequence
 CC encoding hCHT, is useful for expressing hCHT recombinantly. The hCHT
 CC polynucleotide sequence when delivered to a cell, increases cholinergic
 CC function in the cell that is in a patient having Parkinson's disease,
 CC Huntington's disease, Alzheimer's disease, schizophrenia, dysautonomia or
 CC myasthenia gravis. The hCHT antibody is useful for controlling
 CC transporter CHT proteins to the brain, and for treating the above
 CC mentioned diseases. The antibody is also useful for diagnosing the above
 CC mentioned disorders and to detect the influence of cholinergic
 CC signalling. The present sequence represents a bacterial artificial
 CC chromosome (BAC) sequence containing the hCHT gene. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov.
 XX
 SQ Sequence 119040 BP; 37072 A; 22876 C; 21708 G; 36882 T; 0 U; 502 Other;

Query Match 36.2%; Score 630.8; DB 9; Length 119040;
 Best Local Similarity 99.7%; Pred. No. 7.1e-172;
 Matches 632; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1110 AAATGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTTTGTGTTTGGAGC 1169
 | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 30755 ACAGGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTTTGTGTTTGGAGC 30814

 Qy 1170 ATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTC 1229
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 30815 ATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTC 30874

 Qy 1230 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 1289
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 30875 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 30934

Qy	1290	CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG	1349
Db	30935	CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGG	30994
Qy	1350	GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA	1409
Db	30995	GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA	31054
Qy	1410	TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCCTTAAC	1469
Db	31055	TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCCTTAAC	31114
Qy	1470	CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA	1529
Db	31115	CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA	31174
Qy	1530	ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT	1589
Db	31175	ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT	31234
Qy	1590	TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG	1649
Db	31235	TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG	31294
Qy	1650	CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC	1709
Db	31295	CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC	31354
Qy	1710	AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA	1743
Db	31355	AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA	31388

RESULT 14

ADD50651

ID ADD50651 standard; DNA; 142299 BP.

XX

AC ADD50651;

XX

DT 15-JAN-2004 (first entry)

XX

DE BAC sequence #2 containing hCHT DNA.

XX

KW Human; high-affinity choline transporter; hCHT; chromosome 2q12;

KW cholinergic function; Parkinson's disease; Huntington's disease;

KW Alzheimer's disease; schizophrenia; dysautonomia; myasthenia gravis;

KW brain; cholinergic signalling; antiparkinsonian; anticonvulsant;

KW nootropic; neuroprotective; neuroleptic; bacterial artificial chromosome;

KW BAC; ds.

XX

OS Homo sapiens.

XX

PN US2003114399-A1.

XX

PD 19-JUN-2003.

XX


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Qy      1350 GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 1409
          |||
Db      94913 GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 94972

Qy      1410 TGGTATATATAATCAGAAATTTCCATTTAAAACACTTGCCATGGTTACATCATTCTTAAC 1469
          |||
Db      94973 TGGTATATATAATCAGAAATTTCCATTTAAAACACTTGCCATGGTTACATCATTCTTAAC 95032

Qy      1470 CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA 1529
          |||
Db      95033 CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA 95092

Qy      1530 ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT 1589
          |||
Db      95093 ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT 95152

Qy      1590 TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG 1649
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Db      95153 TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG 95212

Qy      1650 CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 1709
          |||
Db      95213 CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 95272

Qy      1710 AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 1743
          |||
Db      95273 AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 95306

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RESULT 15

AAF81710

ID AAF81710 standard; cDNA; 1731 BP.

XX

AC AAF81710;

XX

DT 01-JUN-2001 (first entry)

XX

DE C. elegans high affinity choline transporter protein encoding cDNA.

XX

KW High affinity choline transporter; cho-1; Alzheimer's disease; diagnosis;
KW ss.

XX

OS Caenorhabditis elegans.

XX

FH Key Location/Qualifiers

FT CDS 1. .1731

FT /*tag= a

FT /product= "high affinity choline transporter"

XX

PN WO200116315-A1.

XX

PD 08-MAR-2001.

XX

PF 18-AUG-2000; 2000WO-JP005545.

XX

PR 27-AUG-1999; 99JP-00240642.

PR 27-DEC-1999; 99JP-00368991.

27-DEC-1999; 99JP-00368991.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Query Match 20.9%; Score 363.8; DB 4; Length 1731;
Best Local Similarity 55.1%; Pred. No. 5.5e-95;
Matches 862; Conservative 0; Mismatches 637; Indels 66; Gaps 5;

[illegible]

Db 370 GGCCAACGAATCGGTGGCTTGATGTATGTTCCAGCACTTCTTGGTGAAACATTCTGGACA 429

Qy 427 GCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGATATGCAC 486
 ||||| ||| | || | | || | | | | | | | | | | | | |

Db 430 GCAGCCATTCTTTTCGGCACTTGGTGCAACACTGTCGGTAATTCTTGAATCGACATGAAT 489

Qy 487 ATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTAT 546
 || || | | | || | | | ||||| | ||||| | | || | ||||

Db 490 GCATCAGTGACCCTGTGCGCCTGTATTGCCGTATTCTACACATTCACCGGTGGATACTAT 549

Qy 547 TCTGTGGCCTACACTGATGTGCTTCAGCTCTTTTGCATTTTGTAGGGCTGTGGATCAGC 606
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Db 550 GCAGTCGCGTACACTGACGTGCTTCAACTATTTTGCATTTTCGTGCGTTTGTGGGTTTGC 609

Qy 607 GTCCCTTTGCATTGTGCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTGCATGCC 666
 || || || || | || | | || | | | || | | || |

Db 610 GTGCCGCGGCTATGGTGCATGATGGTGCAGGATATTTCCAGGAATGCAG----- 661

Qy 667 AAATACCAAAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGGCTTGAT 726
 | | | | | | | | | | | | | | | | | | | | |

Db 662 -----GCGACTGGATTGGAGAGATTGGAGGATTCAAAGAAACATCTCTCTGGATTGAT 714

Qy 727 AGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGGGTTCTC 786
 | | || | | | | || ||||| ||||| || || |||||

Db 715 TGCATGCTTCTCCTTGTCTTTGGAGGAATTCCATGGCAAGTGTACTTCCAAAGAGTTCTC 774

Qy 787 TCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCTTCCTGGCAGCTTTCGGGTGCTCG 846
 || || | || | || || | |||| | | || | | |||| || |

Db 775 TCCTCAAAAAGTCTCATGGAGCACAGACGTTGTGCTTGTGGCGGGCGTCGGATGCATT 834

Qy 847 GTGATGGCCATCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGGAACCAG 906
 | ||||| || ||| | | || || || || |||| | ||||| || |

Db 835 CTCATGGCGATTCCACCAGCGTTGATCGGTGCAATTGCCAGGAACACAGACTGGAGAATG 894

Qy 907 ACTGCATATGGGCTTCC-----AGATCCCAAGACTACAGAAGAGGCA 948
 |||| ||| | | | | | || | | | | || || |

Db 895 ACTGATTATTCCCATGGAACAATGGAAGTGAAGTTCGAATCGATTCCACCGGATAAGAGA 954

Qy 949 GACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGT 1008
 ||||| | | || | || | ||||| || | | | ||||

Db 955 AACATGGTGGTCCCGTTGGTATTCCAGTATCTTACGCCAAGATGGGTGCGCTTTATTGGA 1014

Qy 1009 CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGCAAGT 1068
 || || |||| | | ||||| ||||| ||||| || | | |||||

Db 1015 CTCGGCGCAGTGTGCGCTGCTGTAATGTCATCTGCAGATTCTGTACTATCAGCAGCA 1074

Qy 1069 TCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAAGAA 1128
 || ||||| || | ||||| |||| | | | | | || || || |||||

Db 1075 TCAATGTTTGTCTACAACATCTGGAAGCTACAATTGCCCCACGCGTCTGAAAAAGAA 1134

Qy 1129 ATCGTTTGGGTTATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCC 1188
 | | || ||| |||| | | | |||| | |||| | |||||

Db 1135 GTGATAAATTGTGATGAGAATAGCCATCATCTGTGTTGGTATCATGGCAACCATCATGGCA 1194

Qy 1189 TTGCTGACGAAAAGTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTACATCGTT 1248
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Db 1195 CTTACCATTCAAATCCATCTATGGGCTTTGGTATCTTTGTGCAGATTGGTCTACGTCATA 1254

Qy 1249 ATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTG 1308
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 Db 1255 CTCTTCCCTCAACTATTATGTGTTGTATATATGCCACGTAGCAATACGTATGGCTCATTG 1314

Qy 1309 GCAGGTTATGTTTCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTT 1368
 || || |||| || || | | | | |||| |||| | | | ||
 Db 1315 GCTGGCTATGCAGTCGGTCTTGTGCTCCGTTTGATTGGAGGCGAGCCACTTGTATCGCTG 1374

Qy 1369 CAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAA 1428
 | | | | || || || || || || || | || | || |
 Db 1375 CCAGCGTTCTTCCATTATCCAATGTATACGGATGGGG-----TACAGTAT 1419

Qy 1429 TTTCCATTTAAAACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTAT 1488
 || |||| | || | || || | | || | || | || |
 Db 1420 TTCCCATTCAGGACAACCTGCTATGTTATCTTCAATGGCTACTATCTACATTGTATCAATA 1479

Qy 1489 CTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCT 1548
 | | | | || | || || || || || | | || || | |
 Db 1480 CAATCGGAGAAGCTGTTCAAATCGGGACGTTTGTCTCCGGAGTGGGACGTAATGGGTTGT 1539

Qy 1549 GTTGT 1553
 || ||
 Db 1540 GTAGT 1544

Search completed: March 22, 2004, 12:00:55
 Job time : 755 secs

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 11:12:56 ; Search time 144 Seconds
 (without alignments)
 6717.218 Million cell updates/sec

Title: US-10-069-541-5
 Perfect score: 1743
 Sequence: 1 atggcctttccatgtggaagg.....ctgaagataatttacagtga 1743

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	1738.2	99.7	1743	4	US-09-657-252-1	Sequence 1, Appli
2	47.6	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
3	41	2.4	1857	4	US-09-640-198D-3	Sequence 3, Appli
4	41	2.4	2839	4	US-08-595-553A-1	Sequence 1, Appli
5	39.6	2.3	474	4	US-09-621-976-18033	Sequence 18033, A
6	39.2	2.2	1506	4	US-09-328-352-2245	Sequence 2245, Ap
7	39	2.2	558	4	US-09-328-352-3451	Sequence 3451, Ap
8	38.2	2.2	2028	4	US-10-162-012-28	Sequence 28, Appl
9	38.2	2.2	2326	4	US-10-162-012-26	Sequence 26, Appl
c 10	38.2	2.2	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 11	38.2	2.2	1830121	4	US-09-643-990A-1	Sequence 1, Appli

	12	38	2.2	1932	4	US-09-640-198D-1	Sequence 1, Appli
	13	37.4	2.1	4344	4	US-09-601-198-165	Sequence 165, App
c	14	36.6	2.1	4160	4	US-09-134-218-1	Sequence 1, Appli
	15	36.6	2.1	148567	4	US-09-801-876B-3	Sequence 3, Appli
	16	36.6	2.1	148567	4	US-10-254-869-3	Sequence 3, Appli
	17	35.6	2.0	447	4	US-09-621-976-12063	Sequence 12063, A
c	18	35.6	2.0	2397	4	US-09-221-017B-272	Sequence 272, App
	19	35.2	2.0	1461	4	US-09-543-681A-2066	Sequence 2066, Ap
	20	35.2	2.0	2238	1	US-07-841-651-1	Sequence 1, Appli
	21	34.8	2.0	902	4	US-09-671-317-37	Sequence 37, Appl
	22	34.8	2.0	1593	4	US-09-134-001C-1673	Sequence 1673, Ap
c	23	34.8	2.0	12482	4	US-09-512-563C-25	Sequence 25, Appl
c	24	34.8	2.0	25002	4	US-08-961-527-48	Sequence 48, Appl
	25	34.8	2.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	26	34.6	2.0	561	4	US-09-107-532A-3215	Sequence 3215, Ap
	27	34.6	2.0	1005	4	US-09-107-532A-3570	Sequence 3570, Ap
	28	34.6	2.0	2847	4	US-09-484-970B-22	Sequence 22, Appl
c	29	34.6	2.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
	30	34.2	2.0	1515	4	US-09-071-035-431	Sequence 431, App
	31	34.2	2.0	1803	4	US-09-071-035-429	Sequence 429, App
c	32	34	2.0	1109	4	US-08-956-171E-222	Sequence 222, App
c	33	34	2.0	392000	4	US-10-027-983-11	Sequence 11, Appl
c	34	33.8	1.9	369	4	US-09-543-681A-628	Sequence 628, App
c	35	33.8	1.9	3172	1	US-07-741-940-3	Sequence 3, Appli
c	36	33.8	1.9	3172	1	US-08-289-548A-3	Sequence 3, Appli
c	37	33.8	1.9	3172	1	US-08-452-654-3	Sequence 3, Appli
c	38	33.8	1.9	3172	1	US-08-452-655B-3	Sequence 3, Appli
c	39	33.8	1.9	3172	3	US-08-450-582-3	Sequence 3, Appli
c	40	33.8	1.9	3172	4	US-08-449-731-3	Sequence 3, Appli
	41	33.8	1.9	176373	3	US-09-128-155-17	Sequence 17, Appl
	42	33.6	1.9	84495	4	US-09-797-906-3	Sequence 3, Appli
	43	33.4	1.9	1626	4	US-09-328-352-602	Sequence 602, App
	44	33.4	1.9	3593	4	US-09-404-627-3	Sequence 3, Appli
	45	33.4	1.9	4205	4	US-09-404-627-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-657-252-1
; Sequence 1, Application US/09657252
; Patent No. 6500643
; GENERAL INFORMATION:
; APPLICANT: Wu, Dong-Hai
; APPLICANT: Gu, Yunrong
; APPLICANT: Millard, William
; APPLICANT: He, Yun-Je
; TITLE OF INVENTION: Human High Affinity Choline Transporter cDNA
; FILE REFERENCE: MBHB00-639
; CURRENT APPLICATION NUMBER: US/09/657,252
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1743)
US-09-657-252-1

Query Match 99.7%; Score 1738.2; DB 4; Length 1743;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Db	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Db	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Qy	181	ACCTGGGTCCGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	181	ACCTGGGTCCGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTC	420
Db	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTC	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	ATGCACATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Qy	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCCAAATACCAAAAGCCGTGGCTGGGAACTGTTGACTCATCTGAAGTCTACTCTTGG	720

Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Db	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCCTGGCAGCTTTCGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCCTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Db	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA	1080
Qy	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081	CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Qy	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141	ATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Db	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Qy	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441	ACACTTGCCATGGTTACATCATTCCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560
Db	1501	CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA	1560

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 |||
 Db 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 |||
 Db 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680

Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 |||
 Db 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAA 1740

Qy 1741 TGA 1743
 |||
 Db 1741 TGA 1743

RESULT 2

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7218 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   CLONE: pTZgpt-Fls
US-08-232-463-14
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Query Match          2.7%; Score 47.6; DB 1; Length 7218;
Best Local Similarity 6.0%; Pred. No. 0.00054;
Matches    23; Conservative 200; Mismatches 159; Indels    0; Gaps    0;
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Qy      692 CTGTTGACTCATCTGAAGTCTACTCTTGGCTTGATAGTTTCTGTTGTTGATGCTGGGTG 751
      :: :: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db      1088 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1147

Qy      752 GAATCCCATGGCAAGCATACTTTTCAGAGGGTTCTCTCTTCTCCTCAGCCACCTATGCTC 811
      :::: : : : : :::: :::: :::: :::: :::: :::: ::::
Db      1148 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1207

Qy      812 AAGTGCTGTCCTTCTGCGAGCTTTCGGGTGCCTGGTGATGGCCATCCCAGCCATACTCA 871
      : :: :::: :: : :::: : :: : : : : :::: :: : ::
Db      1208 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1267

Qy      872 TTGGGGCCATTGGAGCATCAACAGACTGGAACCAGACTGCATATGGGCTTCCAGATCCCA 931
      :: :::: : : : : : : : : : : : : : : : : : : : :
Db      1268 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1327

Qy      932 AGACTACAGAAGAGGCAGACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGT 991
      :: : : : : : : : : : : : : : : : : : : : :
Db      1328 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1387

Qy      992 ATATTCTTTCTTTGGTCTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTT 1051
      : :::: :::: : : : : : : : : : : : : : : | || |||||
Db      1388 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTACCAAATCTT 1447

Qy      1052 CCATCTTGTCAGCAAGTTCCAT 1073
      | ||| | | | | || |||
Db      1448 CTATCTCTTTAACTACTTGCAT 1469
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RESULT 3

US-09-640-198D-3

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; Sequence 3, Application US/09640198D
; Patent No. 6586411
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen
; APPLICANT: Kay Whye, Peng
; TITLE OF INVENTION: System for Monitoring the Location of
; TITLE OF INVENTION: Transgenes
; FILE REFERENCE: 07039-295001
; CURRENT APPLICATION NUMBER: US/09/640,198D
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-640-198D-3

Query Match 2.4%; Score 41; DB 4; Length 1857;
Best Local Similarity 49.8%; Pred. No. 0.026;
Matches 104; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Qy      404 TGATGGGAGAAATGTTCTGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCG 463
          || |||      ||| | |   | |       | ||| ||   |   || | | | |
Db      413 TGGTGGCCACGATGCTGTATACAGGCATCGTGATCTACGCGCCTGCGCTCATCCTGAACC 472

Qy      464 TGATCATCGATGTGGATATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGT 523
          | | ||   |||| ||       || || |   | | | | ||||   ||| |||
Db      473 AAGTGACCGGGTTGGACATCTGGGCATCGCTCCTGTCCACAGGAATCATTCGACCTTGT 532

Qy      524 ACACACTGGTGGGAGGGCTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCA 583
          ||||   ||||| ||   | | | |||| ||   || |||||   | ||| | |   |
Db      533 ACACTACCGTGGGTGGTATGAAGGCCGTGGTCTGGACAGATGTGTTCCAGGTGTGGTAA 592

Qy      584 TTTTGTAGGGCTGTGGATCAGCGTCCCC 612
          | | || ||   | ||| | | | | ||
Db      593 TGCTCGTTGGCTTCTGGGTGATCCTGGCC 621
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RESULT 4

US-08-595-553A-1

; Sequence 1, Application US/08595553A
; Patent No. 6391579
; GENERAL INFORMATION:
; APPLICANT: NANCY CARRASCO, ET AL.
; TITLE OF INVENTION: THYROID SODIUM/IODIDE SYMPORTER AND
; TITLE OF INVENTION: NUCLEIC ACID ENCODING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
; MEDIUM TYPE: DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,553A
; FILING DATE: FEBRUARY 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG J. ARNOLD
; REGISTRATION NUMBER: 34,287
; REFERENCE/DOCKET NUMBER: 96700/393

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2839
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: RAT
; INDIVIDUAL ISOLATE: SODIUM/IODIDE SYMPORTER
US-08-595-553A-1

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Query Match          2.4%; Score 41; DB 4; Length 2839;
Best Local Similarity 49.8%; Pred. No. 0.035;
Matches 104; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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Qy      404 TGATGGGAGAAATGTTCTGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCG 463
        || |||   ||| | | | | | | ||| || | | ||| |||
Db      522 TGGTGGCCACGATGCTGTATACAGGCATCGTGATCTACGCGCCTGCGCTCATCCTGAACC 581

Qy      464 TGATCATCGATGTGGATATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGT 523
        | | ||   |||| || | | || | | ||| ||| |||
Db      582 AAGTGACCGGGTTGGACATCTGGGCATCGCTCCTGTCCACAGGAATCATCTGCACCTTGT 641

Qy      524 ACACACTGGTGGGAGGGCTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCA 583
        ||||   ||||| || | | | |||| || || |||| | ||| | | |
Db      642 ACACTACCGTGGGTGGTATGAAGGCCGTGGTCTGGACAGATGTGTTCCAGGTTGTGGTAA 701

Qy      584 TTTTGTAGGGCTGTGGATCAGCGTCCCC 612
        | | || || | ||| | | | | ||
Db      702 TGCTCGTTGGCTTCTGGGTGATCCTGGCC 730

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RESULT 5

US-09-621-976-18033

; Sequence 18033, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 18033

; LENGTH: 474

; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18033

Query Match 2.3%; Score 39.6; DB 4; Length 474;
Best Local Similarity 13.4%; Pred. No. 0.03;
Matches 42; Conservative 134; Mismatches 138; Indels 0; Gaps 0;

Qy 981 CTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGAGTTTCTGCTGCTGTTATGTCATC 1040
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Db 54 SKYCSGSYKKT TTTTWWWWTTT TKGKWARRRMSGGKTTYMMCSKKKTKSCMAGRWKG 113

Qy 1041 AGCAGATTCTTCCATCTTGTCAGCAAGTCCATGTTTGCACGGAACATCTACCAGCTTTC 1100
: : : : : | : : : : : : : | : : : : : | :
Db 114 KYYYSRWYYYCYKGACYMWKRWYCSSCCMMYTKGGGSMWTTTWMRRRKSYKRWTKGK 173

Qy 1101 CTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTTATGCGAATCACAGTGTGTTGT 1160
: : : : | : : : : : | : : : : | : : : : : :
Db 174 KKKKTTWMMMAAMCYTTWRSYWMRRRAAAKTYCYCMMSKTMCCMACCCMMCMRRARS 233

Qy 1161 GTTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTA 1220
: : : | : | : : | : : : | : : : : : : : | : : :
Db 234 CCMRSCMRSYTYMMCYYYMYKGRMYWWWRGGMWKRMYYMYKKKSMWKGSCMWKRAWW 293

Qy 1221 CCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAGCTGCTTTGTGTACTCTTTGT 1280
: : | : : : | : : : | : : : : : : : | : : : : :
Db 294 ARKTTYTTWAWYYTTYKRMCCYYMRKTTYCMMWYSRWWRGSMWTARGAWWMCYWWYYY 353

Qy 1281 TAAGGGAACCAACA 1294
| : : : : : | :
Db 354 MAARKKKYMWAAAA 367

RESULT 6

US-09-328-352-2245

; Sequence 2245, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 2245

; LENGTH: 1506

; TYPE: DNA

; ORGANISM: Acinetobacter baumannii

US-09-328-352-2245

Query Match 2.2%; Score 39.2; DB 4; Length 1506;
Best Local Similarity 51.1%; Pred. No. 0.085;

Matches 92; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```
Qy      1008 TCTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGTCAGCAAG 1067
          ||| | ||| ||| ||||| ||||| || | | | ||| |
Db      1005 TCTAGCTGCTATTTTAGCTGCGGTTATGAGTACATTAAGCTGTCAGCTTTTGGTATGTTTC 1064

Qy      1068 TTCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGA 1127
          | | | | ||| | | | | | ||||| || | |||||
Db      1065 AAGTGCCTAACTGAAGATTTGTACAAAGGCTTCATTCGTAAAAATGCATCTCAAAAAGA 1124

Qy      1128 AATCGTTTGGGTTATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGC 1187
          | || ||||| ||| |||| ||| ||| ||| | |||| | |||
Db      1125 GCTTGTATGGGTTGGGCGTATCATGGTGCTTGCAATTGCCGTTCTAGCAATTGTGCTTGC 1184
```

RESULT 7

US-09-328-352-3451

; Sequence 3451, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328,352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 3451

; LENGTH: 558

; TYPE: DNA

; ORGANISM: Acinetobacter baumannii

US-09-328-352-3451

Query Match 2.2%; Score 39; DB 4; Length 558;

Best Local Similarity 50.3%; Pred. No. 0.051;

Matches 96; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

```
Qy      1455 TACATCATTCCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGG 1514
          || |||| | | ||| | ||| | || | || | ||| ||| |
Db      341 TAAATCAAATGATGCAAATGCTTCATGGCTGATGTTGCAAACCTCAACTTTTCAAGATG 400

Qy      1515 AACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAA 1574
          | | | || || ||| | | | | | ||| || | || | ||
Db      401 GCCGTAGTCATCTGAATGCGGCAAAGCTCAAGGTGAAGTTTCAGAAGCAAGCAGATGGAA 460

Qy      1575 CATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGT 1634
          ||||| || || || | ||| || || | | | ||| |||
Db      461 CATGGAATTTAAACATTTCCAAACACAGAATATTTTCAGTCGTCGGTATCGCATTGGC 520

Qy      1635 GAAGCCACGAC 1645
          ||| |||
Db      521 AAAGTGAAGCC 531
```

RESULT 8

US-10-162-012-28

; Sequence 28, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-012-28

Query Match 2.2%; Score 38.2; DB 4; Length 2028;
Best Local Similarity 46.1%; Pred. No. 0.22;
Matches 239; Conservative 0; Mismatches 273; Indels 7; Gaps 3;

```
Qy      79 TGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAAGCCATCATAGTTGGTGGC 138
      |||| | ||||| | | | | ||| || | | ||| |
Db     126 TGGACTATGGTCCACAGTGAAGACCAAAAGAGACACAGTGAAAGGCTACTTCCTGGCTGA 185

Qy     139 CGAGATATTGGTTTATTGGTTGGTGGATTTA-CCATGACAGCTACCTGGGTCGGAGGAGG 197
      | || |||| | || |||| | | || | || || | ||
Db     186 AGGGAACATGGTGTGGTGGCCAGTGGGTGCATCCTTGTTTGCCAGCAATGTTGGAAGTGG 245

Qy     198 GTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTATGGCCTAGCTTGGGCTCA 257
      || ||| |||| || | || | || | || | || | ||| |
Db     246 ACATTTTCATTGGCCTGGCAGGGTCAGGTGCTGCTACGGGCATTTCTGTA---TCAGCTTA 302

Qy     258 GGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTTGCAAAACCTAT 317
      | || | ||| | | | | |||| || | | ||| | | | ||
Db     303 TGAACCTAATGGCTTGTTTTCTGTGCTGATGTTGGCCTGGATCTTCCTACCCATCTACAT 362

Qy     318 GCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAAATCTATGGAAAACGCAT 377
      | ||| || || | ||| || || ||| || ||| | ||
Db     363 TGCTGGTCAGGTCACCACGATGCCAGAATACCTACGGAAGCGCTTCGGTGGCATCAGAAT 422

Qy     378 GGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTCTGGGCTGCAGCAATTTT 437
      | |||| | | | || | | || ||| || | |
Db     423 CCCCATCATCCTGGCTGTACTCTACCTATTTATCTACATCTTCACCAAGATCTCGGTAGA 482

Qy     438 CTCTGCTTTGGGAGCCACCATCAGCGTGATCATCG---ATGTGGATATGCACATTTCTGT 494
      | | || |||| | ||| | | | |||| || || | | |
Db     483 CATGTATGCAGGTGCCATCTTCATCCAGCAGTCTTCGCACCTGGATCTGTACCTGGCCAT 542

Qy     495 CATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATTCTGTGGC 554
      | || | || | |||| | | || || || | ||||
Db     543 AGTTGGGCTACTGGCCATCACTGCTGTATACACGGTTGCTGGTGGCCTGGCTGCTGTGAT 602

Qy     555 CTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGG 593
      ||||| |||| | | || | || || || ||
Db     603 CTACACGATGCCCTGCAGACGCTGATCATGCTTATAGG 641
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RESULT 9

US-10-162-012-26

; Sequence 26, Application US/10162012

; Patent No. 6682597

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,012

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

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; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 2326
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (178)...(2202)
US-10-162-012-26

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```

Query Match          2.2%;   Score 38.2;   DB 4;   Length 2326;
Best Local Similarity 46.1%;   Pred. No. 0.24;
Matches 239;   Conservative 0;   Mismatches 273;   Indels 7;   Gaps 3;

```

```

Qy      79 TGGAGAACCAAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAAGCCATCATAGTTGGTGGC 138
        |||| |   |||||   | | |   ||| |||   | |   ||| |
Db      303 TGGACTATGGTCCACAGTGAAGACCAAAAGAGACACAGTGAAAGGCTACTTCCTGGCTGA 362

Qy      139 CGAGATATTGGTTTATTGGTTGGTGGATTTA-CCATGACAGCTACCTGGGTCTGGAGGAGG 197

```

```

      | | | | | | | | | | | | | | | | | | | | | |
Db    363 AGGGAACATGGTGTGGTGGCCAGTGGGTGCATCCTTGTTTGCCAGCAATGTTGGAAGTGG 422

Qy    198 GTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTATGGCCTAGCTTGGGCTCA 257
      | | | | | | | | | | | | | | | | | | | | | |
Db    423 ACATTTTCATTGGCCTGGCAGGGTCAGGTGCTGCTACGGGCATTTCTGTA---TCAGCTTA 479

Qy    258 GGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTTGCAAAACCTAT 317
      | | | | | | | | | | | | | | | | | | | | | |
Db    480 TGAACCTAATGGCTTGTTTTCTGTGCTGATGTTGGCCTGGATCTTCCTACCCATCTACAT 539

Qy    318 GCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAAATCTATGGAAAACGCAT 377
      | | | | | | | | | | | | | | | | | | | | | |
Db    540 TGCTGGTCAGGTCACCACGATGCCAGAATACCTACGGAAGCGCTTCGGTGGCATCAGAAT 599

Qy    378 GGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTCTGGGCTGCAGCAATTTT 437
      | | | | | | | | | | | | | | | | | | | | | |
Db    600 CCCCATCATCCTGGCTGTACTCTACCTATTTATCTACATCTTCACCAAGATCTCGGTAGA 659

Qy    438 CTCTGCTTTGGGAGCCACCATCAGCGTGATCATCG---ATGTGGATATGCACATTTCTGT 494
      | | | | | | | | | | | | | | | | | | | | | |
Db    660 CATGTATGCAGGTGCCATCTTCATCCAGCAGTCTTCGCACCTGGATCTGTACCTGGCCAT 719

Qy    495 CATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATTCTGTGGC 554
      | | | | | | | | | | | | | | | | | | | | | |
Db    720 AGTTGGGCTACTGGCCATCACTGCTGTATACACGGTTGCTGGTGGCCTGGCTGCTGTGAT 779

Qy    555 CTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGG 593
      | | | | | | | | | | | | | | | | | | | | | |
Db    780 CTACACGGATGCCCTGCAGACGCTGATCATGCTTATAGG 818

```

RESULT 10

US-09-557-884-1/c

; Sequence 1, Application US/09557884

; Patent No. 6506581

; GENERAL INFORMATION:

; APPLICANT: Fleischmann et al.

; TITLE OF INVENTION: The Nucleotide sequence of

; the Haemophilus influenzae Rd Genome, Fragments

; Thereof, and Uses Thereof

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3 1/2 inch diskette

; COMPUTER: Dell Pentium

; OPERATING SYSTEM: MS DOS v6.22

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/557,884

; FILING DATE: 25-Apr-2000

```

;          CLASSIFICATION: <Unknown>
;
;    PRIOR APPLICATION DATA:
;
;          APPLICATION NUMBER: 08/476,102
;
;          FILING DATE: JUN-5-1995
;
;    ATTORNEY/AGENT INFORMATION:
;
;          NAME: Michelle S. Marks
;
;          REGISTRATION NUMBER: 41,971
;
;          REFERENCE/DOCKET NUMBER: PB186P3
;
;    TELECOMMUNICATION INFORMATION:
;
;          TELEPHONE: 301-309-8504
;
;          TELEFAX: 301-309-8439
;
;    INFORMATION FOR SEQ ID NO: 1:
;
;          SEQUENCE CHARACTERISTICS:
;
;            LENGTH: 1830121 base pairs
;
;            TYPE: nucleic acid
;
;            STRANDEDNESS: double
;
;            TOPOLOGY: linear
;
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

```

```

Query Match          2.2%;  Score 38.2;  DB 4;  Length 1830121;
Best Local Similarity 48.7%;  Pred. No. 19;
Matches 132;  Conservative 0;  Mismatches 138;  Indels 1;  Gaps 1;

```

```

Qy      1009 CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTCAAGT 1068
          ||| || ||| || || || ||| || | | | | || | |
Db      1428785 CTTTCCGCTATTTTAGCAGCAGTAATGAGTACATTAAGTGCAGCAATTGTTAATTCCTCT
1428726

```

```

Qy      1069 TCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAA 1128
          | | || | |||| | || | | | || || || || || ||
Db      1428725 AGCTCAATCACAGAAGATTTCTATAAAGGTTTTATTGCGCCCTAACGCATCTGAAAAAGAG
1428666

```

```

Qy      1129 ATCGTTTGGGTTATGCGAATCACAGTGTTTGTGTTTGGAGCATCTGCAACAGCCATGGC- 1187
          |||| ||| || |||| | |||| || || || || || || ||
Db      1428665 CTCGTATGGCTTGGCAGAATTATGGTGTTAGTTATTGCCGCACTTGCTATCTGGATCGCA
1428606

```

```

Qy      1188 CTTGCTGACGAAAACGTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGT 1247
          | | ||| | | | |||| | || || || | | || | ||
Db      1428605 CAAGATGAAAACAGCAAAGTATTAAACTTGTAGAATTTGCTTGGGCGGGGTTGGTAGT
1428546

```

```

Qy      1248 TATCTTCCCCCAGCTGCTTTGTGTACTCTTT 1278
          || ||| | || | | |||||
Db      1428545 GCATTGGCCCTGTTGTACTTTTCTCTCTTT 1428515

```

```

RESULT 11
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
;
;    GENERAL INFORMATION:
;
;          APPLICANT: Robert D. Fleischmann
;
;          Mark D. Adams
;
;          Owen White

```

```

;           Hamilton O. Smith
;           J. Craig Venter
;   TITLE OF INVENTION: The Nucleotide sequence of
;                       the Haemophilus influenzae Rd Genome, Fragments
;                       Thereof, and Uses Thereof
;   NUMBER OF SEQUENCES: 1
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Human Genome Sciences, Inc.
;       STREET: 9410 Key West Avenue
;       CITY: Rockville,
;       STATE: MD
;       COUNTRY: USA
;       ZIP: 20850
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: 3 1/2 inch diskette
;       COMPUTER: Dell Pentium
;       OPERATING SYSTEM: MS DOS v6.22
;       SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/643,990A
;       FILING DATE: 23-Aug-2000
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/487,429
;       FILING DATE: 1995-06-07
;       APPLICATION NUMBER: 08/426,787
;       FILING DATE: 1995-04-21
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Kenley K. Hoover
;       REGISTRATION NUMBER: 40,302
;       REFERENCE/DOCKET NUMBER: PB186P1C1
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 301-610-5790
;       TELEFAX: 310-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1830121 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

```

```

Query Match          2.2%;  Score 38.2;  DB 4;  Length 1830121;
Best Local Similarity 48.7%;  Pred. No. 19;
Matches 132;  Conservative 0;  Mismatches 138;  Indels 1;  Gaps 1;

```

```

Qy      1009 CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTCAGCAAGT 1068
          |||  ||  |||  || || || |||  ||  |  |  |  | ||  |  |
Db      1428785 CTTTCCGCTATTTTAGCAGCAGTAATGAGTACATTAAGTGCGCAATTGTTAATTTCTCT
1428726

Qy      1069 TCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAA 1128
          |  |  ||  |  |||  |  ||  |  |  |  |  ||  ||  |||  |||
Db      1428725 AGCTCAATCACAGAAGATTTCTATAAAGGTTTATTCGCCCTAACGCATCTGAAAAAGAG
1428666

```


Qy 1129 ATCGTTTGGGTTATGCGAATCACAGTGTGTTGTGTTTGGAGCATCTGCAACAGCCATGGC- 1187
 |||| ||| || |||| | |||| || || || || || ||
 Db 1428665 CTCGTATGGCTTGGCAGAATTATGGTGTAGTTATTGCCGCACTTGCTATCTGGATCGCA
 1428606

Qy 1188 CTTGCTGACGAAAACCTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTACATCGT 1247
 | | ||| | | |||| || ||| || | | || | ||
 Db 1428605 CAAGATGAAAACAGCAAAGTATTAACCTTGTAGAATTTGCTTGGGCGGGTTTGGTAGT
 1428546

Qy 1248 TATCTTCCCCCAGCTGCTTTGTGTACTCTTT 1278
 || ||| || | | |||||
 Db 1428545 GCATTTGGCCCTGTTGTACTTTTCTCTCTTT 1428515

RESULT 12

US-09-640-198D-1

; Sequence 1, Application US/09640198D
 ; Patent No. 6586411
 ; GENERAL INFORMATION:
 ; APPLICANT: Russell, Stephen
 ; APPLICANT: Kay Whye, Peng
 ; TITLE OF INVENTION: System for Monitoring the Location of
 ; TITLE OF INVENTION: Transgenes
 ; FILE REFERENCE: 07039-295001
 ; CURRENT APPLICATION NUMBER: US/09/640,198D
 ; CURRENT FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: US 60/149,168
 ; PRIOR FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1932
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-09-640-198D-1

Query Match 2.2%; Score 38; DB 4; Length 1932;
 Best Local Similarity 51.8%; Pred. No. 0.24;
 Matches 86; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 437 TCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGATATGCACATTTCTGTCA 496
 ||| || || ||| ||| || | ||| || || ||
 Db 446 TCTACGCACCGGCCCTCATCTGAACCAAGTGACCGGGCTGGACATCTGGGCGTCGCTCC 505

Qy 497 TCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATTCTGTGGCCT 556
 | | | | | || ||| | |||| |||| || | | ||||| ||
 Db 506 TGTCCACCGGAATTATCTGCACCTTCTACACGGCTGTGGCGGCATGAAGGCTGTGGTCT 565

Qy 557 ACACTGATGTGCTTCAGCTCTTTTGCAATTTTGTAGGGCTGTGGAT 602
 ||||| || | ||| || | || | || | ||| |
 Db 566 GGACTGATGTGTTCCAGGTCGTGGTGATGCTAAGTGGCTTCTGGGT 611

RESULT 13

US-09-601-198-165

; Sequence 165, Application US/09601198

```
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellson Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 165
; LENGTH: 4344
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-165
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Query Match          2.1%; Score 37.4; DB 4; Length 4344;
Best Local Similarity 48.0%; Pred. No. 0.64;
Matches 107; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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Qy      1521 GCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGA 1580
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Db      984 AAGTAACTTATTAGAAATTTTGAAACTAATGAAATTACAAATAATGAATGAAACCAATT 1043

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RESULT 14

US-09-134-218-1/c

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; Sequence 1, Application US/09134218A
; Patent No. 6312926
; GENERAL INFORMATION:
; APPLICANT: Shatkin, Aaron J.
; APPLICANT: Pillutla, Renuka
; APPLICANT: Reinberg, Danny
; APPLICANT: Yu, Zheng
; APPLICANT: Moldanado, Edio
; TITLE OF INVENTION: mRNA CAPPING ENZYMES AND USES THEREOF
; FILE REFERENCE: 601-1-079 ss
; CURRENT APPLICATION NUMBER: US/09/134,218A
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; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4160
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-134-218-1
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Best Local Similarity 46.6%; Pred. No. 1.1;
Matches 117; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
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Qy      1477 TGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAAATTAGAT 1536
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Qy      1537 GTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAATTCTTGTC 1596
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RESULT 15

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US-09-801-876B-3
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3
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Query Match 2.1%; Score 36.6; DB 4; Length 148567;
Best Local Similarity 46.1%; Pred. No. 12;
Matches 123; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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Qy      1536 TGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAAACATGGATAAGACAATTCTTGT 1595
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Db      31913 CCTATAAAAATCACAAACCCAGAAGGA 31939
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Job time : 161 secs

OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 11:50:14 ; Search time 635 Seconds
(without alignments)
10153.739 Million cell updates/sec

Title: US-10-069-541-5
Perfect score: 1743
Sequence: 1 atggctttccatgtggaagg.....ctgaagataatttacagtga 1743

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1743	100.0	1743	10	US-09-911-077A-1	Sequence 1, Appli
2	1743	100.0	1813	10	US-09-911-077A-9	Sequence 9, Appli
3	1394.2	80.0	4904	10	US-09-911-077A-5	Sequence 5, Appli
4	1375	78.9	1743	10	US-09-911-077A-3	Sequence 3, Appli
5	1375	78.9	1743	10	US-09-911-077A-23	Sequence 23, Appl
6	630.8	36.2	119040	10	US-09-911-077A-19	Sequence 19, Appl
7	630.8	36.2	142299	10	US-09-911-077A-14	Sequence 14, Appl
8	376.6	21.6	1833	12	US-10-241-784-1	Sequence 1, Appli
9	363.8	20.9	1985	10	US-09-911-077A-7	Sequence 7, Appli
10	242.6	13.9	1461	9	US-09-974-300-501	Sequence 501, App
c 11	180.8	10.4	119040	10	US-09-911-077A-19	Sequence 19, Appl
c 12	180.8	10.4	142299	10	US-09-911-077A-14	Sequence 14, Appl
13	155	8.9	455	9	US-09-864-761-1838	Sequence 1838, Ap
c 14	118.6	6.8	943	15	US-10-027-632-120553	Sequence 120553,
15	72	4.1	96	9	US-09-864-761-18589	Sequence 18589, A
16	60	3.4	60	10	US-09-908-975-10249	Sequence 10249, A
17	53.8	3.1	65	10	US-09-908-975-26842	Sequence 26842, A
18	41	2.4	1857	15	US-10-428-868-3	Sequence 3, Appli
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c 20	39.8	2.3	666	15	US-10-027-632-137101	Sequence 137101,
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c 23	39.4	2.3	578	15	US-10-027-632-192644	Sequence 192644,
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29	38.2	2.2	2326	15	US-10-162-102-26	Sequence 26, Appl
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33	38	2.2	1932	15	US-10-428-868-1	Sequence 1, Appli
c 34	37.8	2.2	6306	14	US-10-239-676-129	Sequence 129, App
c 35	37.6	2.2	867	12	US-10-142-426-20	Sequence 20, Appl
c 36	37.6	2.2	867	14	US-10-123-155-20	Sequence 20, Appl
c 37	37.6	2.2	867	14	US-10-146-731-20	Sequence 20, Appl
c 38	37.6	2.2	867	14	US-10-140-472-20	Sequence 20, Appl
c 39	37.6	2.2	867	14	US-10-141-761-20	Sequence 20, Appl
c 40	37.6	2.2	867	14	US-10-142-885-20	Sequence 20, Appl
c 41	37.6	2.2	867	14	US-10-158-790-20	Sequence 20, Appl
c 42	37.6	2.2	867	15	US-10-137-871-20	Sequence 20, Appl
c 43	37.6	2.2	867	15	US-10-140-923-20	Sequence 20, Appl
c 44	37.6	2.2	867	15	US-10-141-756-20	Sequence 20, Appl
c 45	37.6	2.2	867	15	US-10-141-759-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-911-077A-1

; Sequence 1, Application US/09911077A

; Publication No. US20030114399A1

; GENERAL INFORMATION:

; APPLICANT: BLAKELY, RANDY D.

```
; APPLICANT: APPARSUNDARAM, SUBRAMANIAM
; APPLICANT: FERGUSON, SHAWN
; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA
; FILE REFERENCE: VBLT:008US
; CURRENT APPLICATION NUMBER: US/09/911,077A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1743)
US-09-911-077A-1
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Query Match          100.0%; Score 1743; DB 10; Length 1743;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCAGTGTGTG	660
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Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
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Qy	1321	TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
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US-09-911-077A-9

; Sequence 9, Application US/09911077A

; Publication No. US20030114399A1

; GENERAL INFORMATION:

; APPLICANT: BLAKELY, RANDY D.

; APPLICANT: APPARSUNDARAM, SUBRAMANIAM

; APPLICANT: FERGUSON, SHAWN

; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA

; FILE REFERENCE: VBLT:008US

; CURRENT APPLICATION NUMBER: US/09/911,077A

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 1813

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (19)..(1761)

US-09-911-077A-9

Query Match 100.0%; Score 1743; DB 10; Length 1813;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1743; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 139 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCT 198

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 |||

Db 679 CATGCCAAATACCAAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG 738

Qy 721 CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTAGAGG 780
 |||

Db 739 CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTAGAGG 798

Qy 781 GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGTCTCCTTCTGGCAGCTTTCGGG 840
 |||

Db 799 GTTCTCTCTTCTTCTCAGCCACCTATGCTCAAGTGTCTCCTTCTGGCAGCTTTCGGG 858

Qy 841 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG 900
 |||

Db 859 TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG 918

Qy 901 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 960
 |||
 Db 919 AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA 978

Qy 961 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1020
 |||
 Db 979 CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT 1038

Qy 1021 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1080
 |||
 Db 1039 TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCCATGTTTGCA 1098

Qy 1081 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1140
 |||
 Db 1099 CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT 1158

Qy 1141 ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1200
 |||
 Db 1159 ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA 1218

Qy 1201 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1260
 |||
 Db 1219 ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG 1278

Qy 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 |||
 Db 1279 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1338

Qy 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
 |||
 Db 1339 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1398

Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 |||
 Db 1399 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1458

Qy 1441 ACACTTGCCATGGTTACATCATTTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 |||
 Db 1459 ACACTTGCCATGGTTACATCATTTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1518

Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 |||
 Db 1519 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1578

Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 |||
 Db 1579 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1638

Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 |||
 Db 1639 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1698

Qy 1681 GAGGCCTTCCTTGATGTTGATTCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 |||
 Db 1699 GAGGCCTTCCTTGATGTTGATTCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1758

Qy	1741	TGA	1743
Db	1759	TGA	1761

RESULT 3

US-09-911-077A-5

; Sequence 5, Application US/09911077A

; Publication No. US20030114399A1

; GENERAL INFORMATION:

APPLICANT: BLAKELY, RANDY D.

; APPLICANT: APPARSUNDARAM, SUBRAMANIAM

APPLICANT: FERGUSON, SHAWN

10 TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA

: FILE REFERENCE: VBLT:008US

; CURRENT APPLICATION NUMBER: US/09/911,077A

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEO ID NOS: 27

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; SOFTWARE: PatentIn Ver. 2.1
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; SEO ID NO 5

; LENGTH: 4904

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (224)..(1966)

US-09-911-077A-5

Query Match 80.0%; Score 1394.2; DB 10; Length 4904;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

Qy	1	ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG	60
Db	224	ATGCCTTTCCATGTAGAAGGACTAGTAGCGATTATCCTGTTCTACCTTCTTATATTTCTG	283
Qy	61	GTTGGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA	120
Db	284	GTTGGAATATGGGCTGCATGGAAAACCAAAAACAGCGTAATGCAGAAGAACGCAGCGAA	343
Qy	121	GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT	180
Db	344	GCCATCATAGTTGGGGCCGAGACATTGGTTTGTGGTTGGTGGTTTACCATGACAGCC	403
Qy	181	ACCTGGGTCGGAGGAGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTAT	240
Db	404	ACCTGGGTTGGAGGAGTTACATCAACGGGACAGCTGAAGCAGTTTATGGGCCAGGTTGT	463
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTAGTCTGATTTTAGGTGGCCTG	300
Db	464	GGTCTAGCTTGGGCTCAGGCACCCATTGGATATTCTCTGAGTCTGATTTTAGGTGGCCTG	523
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	524	TTTTTTGCAAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCGTTTCAACAG	583
Qy	361	ATCTATGGAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTTC	420

Db	584		ATCTATGGAAAGCGCATGGGTGGGCTGCTGTTTCATCCCTGCACTGATGGGAGAGATGTTTC	643
Qy	421		TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	644		TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCTACCATCAGCGTAATCATTGATGTGGAT	703
Qy	481		ATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	704		GTGAACATATCGGTCATTGTCTCCGCACTCATTGCCATTCTTTATACCCTCGTGGGAGGG	763
Qy	541		CTCTATTCTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCAATTTTGTAGGGCTGTGG	600
Db	764		CTCTACTCTGTGGCATATACTGATGTGTACAGCTATTCTGCATTTTATAGGATTGTGG	823
Qy	601		ATCAGCGTCCCCTTTGCATTGTACATCCTGCAGTCGCAGACATCGGGTTCAGTGCTGTG	660
Db	824		ATCAGTGTCCCATTTGCCCTGTACATCCTGCAGTCACCGACATTGGATTCACTGCTGTG	883
Qy	661		CATGCCAAATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCTTGG	720
Db	884		CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATGAATCAGTTGAAGTCTACACCTGG	943
Qy	721		CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	944		CTTGATAATTTTCTGTTGTTGATGCTGGGTGGAATACCATGGCAAGCCTACTTCCAGAGG	1003
Qy	781		GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCTTCCTGGCAGCTTTCGGG	840
Db	1004		GTCTCTCTTCATCGTCAGCGACCTATGCTCAGGTGCTGTCTTCCTGGCAGCTTTTGGG	1063
Qy	841		TGCCTGGTGATGGCCATCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	1064		TGCCTGGTGATGGCTCTACCAGCCATTGTCATTGGGGCCATTGGAGCCTCCACAGACTGG	1123
Qy	901		AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	1124		AACCAAACTGCATATGGGTTTCCAGATCCCAAGACCAAGGAGGAAGCAGACATGATTCTC	1183
Qy	961		CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	1184		CCGATTGTTCTACAGTACCTCTGCCCTGTGTACATTTCTTTCTTTGGGCTTGGTGTCTGTT	1243
Qy	1021		TCTGCTGCTGTTATGTCTCATCAGCAGATTCTTCCATCTTGTCTAGCAAGTTCCATGTTTGCA	1080
Db	1244		TCTGCTGCTGTCTATGTCTCGGCTGACTCATCCATCCTATCAGCAAGTTCCATGTTTGCT	1303
Qy	1081		CGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1304		CGGAATATCTACCAGCTTTCCTTCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1363
Qy	1141		ATGCGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1364		ATGAGGATCACTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTCACGAAG	1423
Qy	1201		ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAG	1260

Db 1424 ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGTCTACATCATCATCTTCCCACAG 1483
 Qy 1261 CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT 1320
 ||||| ||||| ||||| | || ||||| ||||| || || ||||| ||
 Db 1484 CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT 1543
 Qy 1321 TCTGGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC 1380
 | ||| || ||||| ||||| || ||||| ||||| || | ||||| |||
 Db 1544 TTTGGACTTTTCCTGAGAATTACCGGAGGAGAGCCATATCTATACTTGCAGCCCTTAATC 1603
 Qy 1381 TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA 1440
 ||||| ||||| ||||| | ||||| ||||| ||||| || ||||| ||
 Db 1604 TTCTACCCTGGTTATTACCCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA 1663
 Qy 1441 ACACTTGCCATGGTTACATCATCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT 1500
 || || ||||| ||||| ||||| ||||| | ||||| ||||| |||||
 Db 1664 ACTCTCTCCATGGTTACCTCATCTTTACCAACATTTGTGTTTCCTATCTAGCCAAGTAT 1723
 Qy 1501 CTATTTGAAAGTGGAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTTGCAAGA 1560
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
 Db 1724 CTATTTGAAAGTGGAACCTTGCCCTCCAAAATTAGATATATTTGATGCTGTTGTCTCAAGG 1783
 Qy 1561 CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT 1620
 ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||
 Db 1784 CACAGTGAAGAGAACATGGACAAGACCATTCTAGTCAGAAATGAAAACATCAAATTAAAT 1843
 Qy 1621 GAACTTGCACTTGTGAAGCCACGACAGAGCATGACCCTCAGCTCAACTTTCACCAATAAA 1680
 ||||| ||| ||||| ||||| | ||||| ||||| ||||| |||||
 Db 1844 GAACTTGCACTGTAAAGCCTCGACAGAGCCTAACCCCTCAGTTCAACTTTCACCAATAAA 1903
 Qy 1681 GAGGCCTTCCTTGATGTTGATTCCAGTCCAGAAGGGTCTGGGACTGAAGATAATTTACAG 1740
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 1904 GAGGCTCTCCTTGATGTTGATTCCAGTCCAGAGGGATCTGGGACTGAAGATAAATTACAA 1963
 Qy 1741 TGA 1743
 |||
 Db 1964 TGA 1966

RESULT 4

US-09-911-077A-3

; Sequence 3, Application US/09911077A

; Publication No. US20030114399A1

; GENERAL INFORMATION:

; APPLICANT: BLAKELY, RANDY D.

; APPLICANT: APPARSUNDARAM, SUBRAMANIAM

; APPLICANT: FERGUSON, SHAWN

; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA

; FILE REFERENCE: VBLT:008US

; CURRENT APPLICATION NUMBER: US/09/911,077A

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 1743

; TYPE: DNA

; ORGANISM: Mus musculus

Qy	721	CTTGATAGTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721		
Qy	781	CTTGATAATTTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG	780
Qy	781	GTTCTCTCTTCTTCTCCTCAGCCACCTATGCTCAAGTGCTGTCTTCTTGGCAGCTTTCGGG	840
Db	781		
Qy	841	GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTAAGTGCTTCTTGGCAGCTTTTGGG	840
Qy	841	TGCCTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841		
Qy	901	TGCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901		
Qy	961	AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATTCTC	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCA	1020
Db	961		
Qy	1021	CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGCTGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTCCATGTTTGCA	1080
Db	1021		
Qy	1081	TCAGCTGCTGTCATGTCCTCAGCTGACTCGTCCATCCTGTGCGGAGTTCTATGTTTGCT	1080
Qy	1081	CGGAACATCTACCAGCTTTCTTCCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTT	1140
Db	1081		
Qy	1141	CGGAATATCTACCAGCTTTCTTCCAGACAAAATGCATCAGACAAGGAAATTGTGTGGGTC	1140
Qy	1141	ATGCGAATCAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAA	1200
Db	1141		
Qy	1201	ATGAGGATCACTGTGCTTGTGTTTCGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAG	1200
Qy	1201	ACTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCAG	1260
Db	1201		
Qy	1261	ACTGTGTATGGGCTCTGGTACCTGAGCTCTGACCTTGTTCTACATCATCATCTTCCCACAG	1260
Qy	1261	CTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTT	1320
Db	1261		
Qy	1321	CTGCTCTGTGTACTCTTCATCAAAGGAACCAACACTTATGGGGCAGTTGCTGGTTATATT	1320
Qy	1321	TCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATC	1380
Db	1321		
Qy	1381	TTTGGACTATTCTGAGAATTACTGGAGGAGAGCCATATCTATACTTGCAGCCCTTAATC	1380
Qy	1381	TTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAA	1440
Db	1381		
Qy	1441	TTCTACCCTGGTTATTACTCTGACAAGAATGGTATATACAATCAGAGGTTCCCATTTAAA	1440
Qy	1441	ACACTTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTAT	1500
Db	1441		
Qy	1501	ACTCTCTCCATGGTTACCTCATTCTTTACCAACATTTGTGTTTCTTATCTAGCCAAGTAT	1500
Qy	1501	CTATTTGAAAGTGGAAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTGCAAGA	1560
Db	1501		
Qy	1561	CTATTTGAAAGTGGAAACCTTGCCACCTAAATTAGATGTATTTGATGCTGTTGTGCAAGG	1560
Qy	1561	CACAGTGAAGAAAACATGGATAAGACAATTCTTGTCAAAAATGAAAATATTAAATTAGAT	1620

Db	181	ACCTGGGTTGGAGGAGGCTACATCAATGGGACAGCAGAAGCAGTGTATGGGCCAGGTTGT	240
Qy	241	GGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTG	300
Db	241	GGTCTAGCTTGGGCTCATGCACCCATTGGATATTCTCTGAGTCTAATTTTAGGTGGTCTG	300
Qy	301	TTCTTTGCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAA	360
Db	301	TTTTTTGCGAAACCTATGCGTTCCAAGGGATATGTGACTATGTTAGACCCATTCAAACAG	360
Qy	361	ATCTATGGAAAACGCATGGGCGGACTCCTGTTTATTCCTGCACTGATGGGAGAAATGTTT	420
Db	361	ATCTATGGAAAGCGCATGGGTGGGCTGCTCTTCATCCCTGCACTGATGGGAGAGATGTTT	420
Qy	421	TGGGCTGCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGAT	480
Db	421	TGGGCTGCAGCAATTTTCTCTGCATTAGGGGCCACCATCAGCGTGATCATTGATGTGGAT	480
Qy	481	ATGCACATTTCTGTCTCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGG	540
Db	481	GTGAACATATCGGTCATTGTCTCTGCACTCATTGCCATTCTTTATACCCTAGTGGGTGGG	540
Qy	541	CTCTATTCTGTGGCCTACACTGATGTCGTTTCTGCTCTTTTGCATTTTGTAGGGCTGTGG	600
Db	541	CTCTACTCTGTGGCATATACTGATGTTGTCCAGCTATTCTGCATTTTATAGGACTGTGG	600
Qy	601	ATCAGCGTCCCCTTTGCATTGTCACATCCTGCAGTCGCAGACATCGGGTTCACTGCTGTG	660
Db	601	ATCAGTGTCCCTTTTGGCCTGTCACATCCTGCAGTCACCGACATCGGATTCACAGCTGTG	660
Qy	661	CATGCCAAATACCAAAGCCGTGGCTGGGAACCTGTTGACTCATCTGAAGTCTACTCTTGG	720
Db	661	CATGCTAAATACCAGAGTCCCTGGCTGGGAACCATTGAATCAGTTGAAGTCTACACCTGG	720
Qy	721	CTTGATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGG	780
Db	721	CTTGATAATTTTCTGTTATTGATGCTGGGTGGAATCCCATGGCAAGCCTACTTCCAGAGG	780
Qy	781	GTTCTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGTCTCCTTCCTGGCAGCTTTCGGG	840
Db	781	GTCCTCTCTTCATCCTCAGCCACCTATGCTCAGGTACTGTCCTTCCTGGCAGCTTTTGGG	840
Qy	841	TGCCCTGGTGATGGCCATCCCAGCCATACTCATTTGGGGCCATTGGAGCATCAACAGACTGG	900
Db	841	TGCCCTGGTGATGGCTCTACCCGCCATATGCATAGGAGCTATTGGAGCTTCCACAGACTGG	900
Qy	901	AACCAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTA	960
Db	901	AACCAGACTGCCTACGGGTATCCAGATCCCAAGACTAAGGAGGAAGCAGACATGATTCCTC	960
Qy	961	CCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTCTTTCTTTGGTCTTGGTGCAGTT	1020
Db	961	CCGATCGTTCTGCAGTACCTCTGCCCTGTGTACATCTCCTTCTTTGGGCTTGGTGTCTGTT	1020
Qy	1021	TCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGTTCATGTTTGCA	1080
Db	1021	TCAGCTGCTGTCATGTCCTCAGCTGACTCGTCCATCCTGTCGGCGAGTTCTATGTTTGCT	1080

Qy 1650 CATGACCCTCAGCTCAACTTTACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 1709
 |||
 Db 31295 CATGACCCTCAGCTCAACTTTACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 31354

Qy 1710 AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 1743
 |||
 Db 31355 AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 31388

RESULT 7

US-09-911-077A-14

; Sequence 14, Application US/09911077A
 ; Publication No. US20030114399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BLAKELY, RANDY D.
 ; APPLICANT: APPARSUNDARAM, SUBRAMANIAM
 ; APPLICANT: FERGUSON, SHAWN
 ; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA
 ; FILE REFERENCE: VBLT:008US
 ; CURRENT APPLICATION NUMBER: US/09/911,077A
 ; CURRENT FILING DATE: 2001-07-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 142299
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Primer
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (1305)..(127835)
 ; OTHER INFORMATION: N = A, C, G or T/U
 US-09-911-077A-14

Query Match 36.2%; Score 630.8; DB 10; Length 142299;
 Best Local Similarity 99.7%; Pred. No. 5.6e-178;
 Matches 632; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1110 AAATGCTTCGGACAAAGAAATCGTTTGGGTATGCGAATCACAGTGTTTGTGTTTGGAGC 1169
 |||
 Db 94673 ACAGGCTTCGGACAAAGAAATCGTTTGGGTATGCGAATCACAGTGTTTGTGTTTGGAGC 94732

Qy 1170 ATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTC 1229
 |||
 Db 94733 ATCTGCAACAGCCATGGCCTTGCTGACGAAACTGTGTATGGGCTCTGGTACCTCAGTTC 94792

Qy 1230 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 1289
 |||
 Db 94793 TGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAAC 94852

Qy 1290 CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCTGAGAATAACTGGAGG 1349
 |||
 Db 94853 CAACACCTATGGGGCCGTGGCAGGTTATGTTTCTGGCCTCTTCTGAGAATAACTGGAGG 94912

Qy 1350 GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 1409

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Db      94913  |||||GGAGCCATATCTGTATCTTCAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAA 94972
Qy      1410  TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCTTAAC 1469
Db      94973  |||||TGGTATATATAATCAGAAATTTCCATTTAAACACTTGCCATGGTTACATCATTCTTAAC 95032
Qy      1470  CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA 1529
Db      95033  |||||CAACATTTGCATCTCCTATCTAGCCAAGTATCTATTTGAAAGTGGAACCTTGCCACCTAA 95092
Qy      1530  ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT 1589
Db      95093  |||||ATTAGATGTATTTGATGCTGTTGTTGCAAGACACAGTGAAGAAAACATGGATAAGACAAT 95152
Qy      1590  TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG 1649
Db      95153  |||||TCTTGTCAAAAATGAAAATATTAAATTAGATGAACTTGCACTTGTGAAGCCACGACAGAG 95212
Qy      1650  CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 1709
Db      95213  |||||CATGACCCTCAGCTCAACTTTCACCAATAAAGAGGCCTTCCTTGATGTTGATTCCAGTCC 95272
Qy      1710  AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 1743
Db      95273  |||||AGAAGGGTCTGGGACTGAAGATAATTTACAGTGA 95306

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RESULT 8

US-10-241-784-1

; Sequence 1, Application US/10241784

; Publication No. US20040048261A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Corporation

; TITLE OF INVENTION: Invertebrate Choline Transporter Nucleic Acid,
Polypeptides and Uses

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: MO7218

; CURRENT APPLICATION NUMBER: US/10/241,784

; CURRENT FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1833

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1833)

; OTHER INFORMATION:

US-10-241-784-1

Query Match 21.6%; Score 376.6; DB 12; Length 1833;

Best Local Similarity 56.0%; Pred. No. 2e-102;

Matches 868; Conservative 0; Mismatches 624; Indels 57; Gaps 6;

Qy 8 TCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTGGTTGGAA 67

Db	5	TCAATATCGCTGGCGTGGTGAGCATCGTGCTCTTCTACCTCCTGATCCTGGTCGTTGGCA	64
Qy	68	TATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAAGCCATCA	127
Db	65	TTTGGGCCGGTCGCAAGAAGCAGTCCGGCAATGATTCGGAGGAG-----GAGGTCA	115
Qy	128	TAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCTACCTGGG	187
Db	116	TGCTGGCCGGACGCTCCATCGGCCTCTTCGTGGGCATCTTCACCATGACGGCCACCTGGG	175
Qy	188	TCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTATGGCCTAG	247
Db	176	TGGGTGGCGGCTACATCAACGGCACGGCGGAGGCTATATACACATCGGGT-----CTGG	229
Qy	248	CTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTTG	307
Db	230	TGTGGTGCCAGGCTCCATTTGGATACGCTCTAAGCTTGGTATTTGGTGGCATCTTCTTTG	289
Qy	308	CAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAAATCTATG	367
Db	290	CCAATCCCATGCGCAAGCAGGGTTACATCACCATGTTGGATCCGTTGCAGGATTCTCTTTG	349
Qy	368	GAAAACGCATGGGCGGACTCCTGTTTATTCTGCACTGATGGGAGAAATGTTCTGGGCTG	427
Db	350	GTGAGCGGATGGGAGGATTGCTCTTCTGCCCGCTCTATGCGGTGAGGTCTTTTGGGCAG	409
Qy	428	CAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGATATGCACA	487
Db	410	CCGGCATCCTGGCTGCACTTGGCGCCACTCTATCGGTGATCATCGACATGGATCACCGCA	469
Qy	488	TTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATT	547
Db	470	CCTCGGTGATCCTGTCTCTGCATCGCCATCTTCTACACACTGTTCCGGTGGACTGTACT	529
Qy	548	CTGTGGCCTACACTGATGTCGTTTCAGCTCTTTTGCATTTTGTAGGGCTGTGGATCAGCG	607
Db	530	CCGTGGCGTATACGGACGTGATCCAGTTGTTCTGCATCTTCATCGGTCTGTGGATGTGCA	589
Qy	608	TCCCCTTTGCATTGTACATCCTGCAGTCGACAGACATCGGGTTCAGTGTGTGCATGCCA	667
Db	590	TTCCCTTCGCCTGGAGCAACGAGCACGTGGGCAGCCTGAGTGACCTGGAGGTGGAT----	645
Qy	668	AATACCAAAAGCCGTGGCTGGGAACGTGTGACTCATCTGAAGTCTACTCTTGGCTTGATA	727
Db	646	-----TGGATTGGGCACGTGGAGCCTAAAAAGCATTGGCTGTACATAGACT	691
Qy	728	GTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGGGTCTCT	787
Db	692	ACGGCTTGCTGCTCGTCTTTGGTGGCATTCCCTGGCAGGTCTACTTCCAGCGGCAAAAC-	750
Qy	788	CTTCTTCTCAGCCACCTATGCTCAAGTGCTGTCTTCTTGGCAGCTTTCGGGTGCCTGG	847
Db	751	-----GGCAGGAAGGGCCAGCTTCTGCCTATGTTGCAGCCGCCGATGCATTT	799
Qy	848	TGATGGCCATCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGGAACCAGA	907

Db	800	TGATGGCCATTCCCCGGTGCTCATCGGAGCGATTGCCAAGGCTACACCTTGGAACGAGA	859
Qy	908	CTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTACCAATTG	967
Db	860	CAGATTACAAGGGACCCTATCCCCTGACCGTGGACGAGACGAGCATGATTCTGCCCATGG	919
Qy	968	TTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTTTCTGCTG	1027
Db	920	TGCTGCAGTACCTCACGCCTGACTTCGTGTCCTTCTTTGGATTGGGCGCTGTTTCCGCCG	979
Qy	1028	CTGTTATGTTCATCAGCAGATTCTTCCATCTTGTCAGCAAGTTCCATGTTTGCACGGAACA	1087
Db	980	CCGTGATGTCCTCCGCCGACTCCTCGGTGCTCTCCGCCGCTCCATGTTGCTCGGAACG	1039
Qy	1088	TCTACCAGCTTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTATGCGAA	1147
Db	1040	TGTACAAATTGATTTTCCGTGAGAAGGCGTCCGAGATGGAAATCATTTGGGTGATGCGAG	1099
Qy	1148	TCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAAACGTGT	1207
Db	1100	TCGCCATCATTGTGGTGGGCATCCTGGCTACCATCATGGCCCTCACCATTCCCTCCATCT	1159
Qy	1208	ATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTTATCTTCCCCCAGCTGCTT-	1266
Db	1160	ACGGTTTGTGGTCCATGTGCTCGGATCTGGTCTACGTCATTCTGTTCCCGCAGCTACTGA	1219
Qy	1267	--TGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTTTCTG	1324
Db	1220	TGGTGGTGCACCTCAAGAAGCACTGCAACACGTACGGCAGCCTGTGCGGCATACATTGTGG	1279
Qy	1325	GCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATCTTCT	1384
Db	1280	CCCTGGCCATCCGACTGTGCGGCGGTGAGGCCATCTGGGACTGGCTCCATTGATCAAGT	1339
Qy	1385	ACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAATTTCCATTTAAACAC	1444
Db	1340	ATCCCGGCTACGACGAGGAGACCAAGG-----AGCAGATGTTCCCCTTCCGCACCA	1390
Qy	1445	TTGCCATGGTTACATCATTCTTAACCAACATTTGCATCTCCTATCTAGCCAAGTATCTAT	1504
Db	1391	TGGCCATGCTGCTCAGCCTGGTCACGCTCATCTCGGTCTCCTGGTGGACTAAAATGATGT	1450
Qy	1505	TTGAAAGTGGAACTTGCCACCTAAATTAGATGTATTTGATGCTGTTGT	1553
Db	1451	TTGAGTCCGGCAAGTTGCCGCCAGCTACGACTACTTCCGCTGTGTGGT	1499

US-09-911-077A-7

; Publication No. US20030114399A1

; APPLICANT: BLAKELY, RANDY D.

; APPLICANT: FERGUSON, SHAWN

; FILE REFERENCE: VBLT:008US


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; CURRENT APPLICATION NUMBER: US/09/911,077A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1739)
US-09-911-077A-7
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Query Match 20.9%; Score 363.8; DB 10; Length 1985;
Best Local Similarity 55.1%; Pred. No. 1.6e-98;
Matches 862; Conservative 0; Mismatches 637; Indels 66; Gaps 5;

Qy	19	GGACTGATAGCTATCATCGTGTTCTACCTTCTAATTTTGTCTGGTTGGAATATGGGCTGCC	78
Db	24	GGTATCGTGGCCATTGTGTTCTTCTACGTGCTCATTCTTGTCGTTGGAATATGGGCGGGT	83
Qy	79	TGGAGAACCAAAA-----ACAGTGGCAGCGCAGAAGAGCGCAGCGAAGCCATC	126
Db	84	AGAAAATCGAAAAGTTCAAAAGAGCTTGAATCAGAAGCCGGCGCGGCGACGGAAGAGGTG	143
Qy	127	ATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTTACCATGACAGCTACCTGG	186
Db	144	ATGTTAGCTGGGAGAAACATCGGAACTCTTGTCGGAATTTTCACAATGACTGCCACGTGG	203
Qy	187	GTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAGGTTATGGCCTA	246
Db	204	GTTGGCGGTGCTTATATCAATGGAACCGCCGAGGCTCTGTATAATGGAGGT-----CTC	257
Qy	247	GCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTT	306
Db	258	CTTGGATGTCAGGCTCCAGTTGGATATGCAATTTCCCTTGTTATGGGAGGACTACTTTTC	317
Qy	307	GCAAAACCTATGCGTTCAAAGGGGTATGTGACCATGTTAGACCCGTTTCAGCAAATCTAT	366
Db	318	GCAAAGAAAATGCGAGAAGAAGGATATATTACAATGCTCGATCCTTTTCAGCACAAATAT	377
Qy	367	GGAAAACGCATGGGCGGACTCCTGTTTATTCCCTGCACTGATGGGAGAAATGTTCTGGGCT	426
Db	378	GGCCAACGAATCGGTGGCTTGATGTATGTTCCAGCACTTCTTGGTGAAACATTCTGGACA	437
Qy	427	GCAGCAATTTTCTCTGCTTTGGGAGCCACCATCAGCGTGATCATCGATGTGGATATGCAC	486
Db	438	GCAGCCATTCTTTCGGCACTTGGTGCAACACTGTCGGTAATTCTTGAATCGACATGAAT	497
Qy	487	ATTTCTGTCATCATCTCTGCACTCATTGCCACTCTGTACACACTGGTGGGAGGGCTCTAT	546
Db	498	GCATCAGTGACCCTGTCGGCCTGTATTGCCGTATTCTACACATTACCGGTGGATACTAT	557
Qy	547	TCTGTGGCCTACACTGATGTCGTTCACTCTTTTGCATTTTGTAGGGCTGTGGATCAGC	606
Db	558	GCACTCGCGTACACTGACGTCGTTCAACTATTTTGCATTTTCGTCGGTTTGTGGGTTTGC	617

Qy	607	GTCCCTTTTGCAATTGTGCATCCTGCAGTCGCAGACATCGGGTTCAGTGCCTGTGCATGCC	666
Db	618	GTGCCGGCGGGCTATGGTGCATGATGGTGCGAAGGATATTTCCAGGAATGCAG-----	669
Qy	667	AAATACCAAAGCCGTGGCTGGGAACGTGTGACTCATCTGAAGTCTACTCTTGGCTTGAT	726
Db	670	-----GCGACTGGATTGGAGAGATTGGAGGATTCAAAGAAACATCTCTCTGGATTGAT	722
Qy	727	AGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGGGTTCTC	786
Db	723	TGCATGCTTCTCCTTGTCTTTGGAGGAATTCCATGGCAAGTGTACTTCCAAAGAGTTCTC	782
Qy	787	TCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGGTGCCTG	846
Db	783	TCCTCAAAACTGCTCATGGAGCACAGACGTTGTCGTTTGTGGCGGGCGTCGGATGCATT	842
Qy	847	GTGATGGCCATCCAGCCATACTCATTTGGGGCCATTGGAGCATCAACAGACTGGAACCAG	906
Db	843	CTCATGGCGATTCCACCAGCGTTGATCGGTGCAATTGCCAGGAACACAGACTGGAGAATG	902
Qy	907	ACTGCATATGGGCTTCC-----AGATCCCAAGACTACAGAAGAGGCA	948
Db	903	ACTGATTATTCCCCATGGAACAATGGAACCTAAGGTCGAATCGATTCCACCGGATAAGAGA	962
Qy	949	GACATGATTTTACCAATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGT	1008
Db	963	AACATGGTGGTCCCGTTGGTATTCCAGTATCTTACGCCAAGATGGGTGCGCTTTATTGGA	1022
Qy	1009	CTTGGTGCAGTTTCTGCTGCTGTTATGTCATCAGCAGATTCTTCCATCTTGTGAGCAAGT	1068
Db	1023	CTCGGCGCAGTGTGCGCTGCTGTAATGTCATCTGCAGATTCTGTACTATCAGCAGCA	1082
Qy	1069	TCCATGTTTGCACGGAACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAA	1128
Db	1083	TCAATGTTTGTCTCACAACATCTGGAAGCTCACAATTCGCCCTCACGCGTCTGAAAAAGAA	1142
Qy	1129	ATCGTTTGGGTATGCGAATCACAGTGTGTTGTGTTTGGAGCATCTGCAACAGCCATGGCC	1188
Db	1143	GTGATAATTGTGATGAGAATAGCCATCATCTGTGTTGGTATCATGGCAACCATCATGGCA	1202
Qy	1189	TTGCTGACGAAAACGTGTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTTTACATCGTT	1248
Db	1203	CTTACCATTCAATCCATCTATGGGCTTTGGTATCTTTGTGCAGATTGGTCTACGTCATA	1262
Qy	1249	ATCTTCCCCCAGCTGCTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTG	1308
Db	1263	CTCTTCCCTCAACTATTATGTGTTGTATATATGCCACGTAGCAATACGTATGGCTCATTG	1322
Qy	1309	GCAGGTATGTTTCTGGCCTCTTCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTT	1368
Db	1323	GCTGGCTATGCAGTCGGTCTTGTGCTCCGTTTGATTGGAGGCGAGCCACTTGTATCGCTG	1382
Qy	1369	CAGCCCTTGATCTTCTACCCTGGCTATTACCCTGATGATAATGGTATATATAATCAGAAA	1428
Db	1383	CCAGCGTTCCTCCATTATCCAATGTATACGGATGGGG-----TACAGTAT	1427
Qy	1429	TTTCCATTTAAACACTTGCCATGGTTACATCATTTCTTAACCAACATTTGCATCTCCTAT	1488

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      || |||| | ||| ||| ||| | ||| | || | | ||
Db      1428 TTCCCATTCAGGACAACTGCTATGTTATCTTCAATGGCTACTATCTACATTGTATCAATA 1487

Qy      1489 CTAGCCAAGTATCTATTTGAAAGTGGAAACCTTGCCACCTAAATTAGATGTATTTGATGCT 1548
      | | | | | | | | | | | | | | | | | | | |
Db      1488 CAATCGGAGAAGCTGTTCAAATCGGGACGTTTGTCTCCGGAGTGGGACGTAATGGGTTGT 1547

Qy      1549 GTTGT 1553
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Db      1548 GTAGT 1552

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RESULT 10

US-09-974-300-501

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; Sequence 501, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 501
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-501

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Query Match          13.9%; Score 242.6; DB 9; Length 1461;
Best Local Similarity 52.4%; Pred. No. 5.9e-62;
Matches 663; Conservative 0; Mismatches 554; Indels 48; Gaps 4;

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Qy      151 TTATTGGTTGGTGGATTTACCATGACAGCTACCTGGGTCGGAGGAGGGTATATCAATGGC 210
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Db      125 TTTTTCGTTCGGAATGGTGACGATGGCCGCAACATGGGTCGGCGCGGATATATTAACGGA 184

Qy      211 ACAGCTGAAGCAGTTTATGTACCAGGTTATGGCCTAGCTTGGGCTCAGGCACCAATTGGA 270
      || || ||| | ||| | | |||| | |||| || || || ||
Db      185 ACGGCCGAATCGACTTACA-----GCGACGGCCTCATCTGGGCCCCAAGCGCCTTGGGGC 238

Qy      271 TATTCTCTTAGTCTGATTTTAGGTGGCCTGTTCTTTGCAAACCTATGCGTTCAAAGGGG 330
      || | | || ||||| | || || | |||| || | | |||| |
Db      239 TACGCATTGAGCCTGATTATCGGCGGTATTTTCTTCGCCAGAAAAATGCGCCGTCATCAA 298

Qy      331 TATGTGACCATGTTAGACCCGTTTCAGCAAATCTATGGAAAACGCATGGGCGGACTCCTG 390
      | | ||||| | || || | | || || || || || || || |
Db      299 TTTATGACCATTATCGATCCTCTCGAACAGCGCTTCGGTAAGCGGATGGCCGGCGTTT 358

Qy      391 TTTATTCTGCACTGATGGGAGAAATGTTCTGGGCTGCAGCAATTTTCTCTGCTTTGGGA 450

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Db 359 TATATACCGGCGCTGTTAGGAGAATTGTTTTGGAGCGCCGCGATCTTAACGGCATTGGGC 418
 Qy 451 GCCACCATCAGCGTGATCATCGATGTGGATATGCACATTTCTGTCATCATCTCTGCACTC 510
 Db 419 ACGACTTTCGGAATGATTCTGAATATCGATTTCCAAACGTCGATTATTTCTTCGGCGATG 478
 Qy 511 ATTGCCACTCTGTACACACTGGTGGGAGGGCTCTATTCTGTGGCCTACACTGATGTCGTT 570
 Db 479 ATCGCCATCGCTTATACGGTGGCCGGAGGCATGTGGGCAGTTGCTTTCACAGATGTCTTT 538
 Qy 571 CAGCTCTTTTGCATTTTTGTAGGGCTGTGGATCAGCGTCCCCTTTGCATTGTCACATCCT 630
 Db 539 CAAATGATTGTCATTTTGTCTGGGCTGTTTTAGTCGTCCCATTTGTATTGTCGAATGTC 598
 Qy 631 GCAG-----TCGCAGACATCGGGTTCAGTGTGCTGTGCATGCCAA 668
 Db 599 GGTGCTCTCGATAGCGTATGGGCAAATTACAGGCACGATTTCCGGCAGCAGCGCCAATCTG 658
 Qy 669 ATACCAAAGCCGTGGCTGGGAAGTGTGACTCATCTGAAGTCTACTCT-----TGGCTT 723
 Db 659 CTTCCGCCGTGGACGGCTGGAAAAACCCGGATTGGGGAAACCTGTTTTGGAAGTGGTGG 718
 Qy 724 GATAGTTTTCTGTTGTTGATGCTGGGTGGAATCCCATGGCAAGCATACTTTTCAGAGGGTT 783
 Db 719 GATAATGCGCTCCTCTTAATTTTCGGAGGTATCGCATGGCAGGTGTACTTTTCAGCGCGTT 778
 Qy 784 CTCTCTTCTTCCTCAGCCACCTATGCTCAAGTGCTGTCTTCCTGGCAGCTTTTCGGGTGC 843
 Db 779 CTTTCGGCAAATTCGGAAGCGCCGCCATGTGGCAGTCGATAATTGCCGGAGTGATCTGC 838
 Qy 844 CTGGTGATGGCCATCCCAGCCATACTCATTGGGGCCATTGGAGCATCAACAGACTGGAAC 903
 Db 839 ATCATTGCCGCCATTCCGTGCGTAATCATCGGAGCTGCCGGAAACAGTACCGATTGGAGC 898
 Qy 904 CAGACTGCATATGGGCTTCCAGATCCCAAGACTACAGAAGAGGCAGACATGATTTTACCA 963
 Db 899 CTGTTTCGGAGCGAGCGCTCCGGATAACCCGGCG-----ATGATTTTGCCG 943
 Qy 964 ATTGTTCTGCAGTATCTCTGCCCTGTGTATATTTCTTTCTTTGGTCTTGGTGCAGTTTCT 1023
 Db 944 CAAACGCTTGCGTATTTGACGCCAGGAATCATCGCAGGCCTCGGCTTGGGTGCAATCGCA 1003
 Qy 1024 GCTGCTGTTATGTATCATCAGCAGATTCTTCCATCTGTGTCAGCAAGTTCATGTTTGACGG 1083
 Db 1004 GCAGCCGTGATGTCAAGCATGGACTCATCGATTCTATCGGCATCATCAATGGCCGCATGG 1063
 Qy 1084 AACATCTACCAGCTTTCCTTCAGACAAAATGCTTCGGACAAAGAAATCGTTTGGGTATG 1143
 Db 1064 AATATTTACCGTCCGCTCATCAAGCCGAAGGCCACCCAAAAACAGCTGCAAAAAGTCGTC 1123
 Qy 1144 CGAATCACAGTGTGTTGTGTTGGAGCATCTGCAACAGCCATGGCCTTGCTGACGAAAACT 1203
 Db 1124 AAACGCTCAATCATTTTGTTCGGCGCGGGAGCAGCGGTGTCGCGCTGAATGTCAAAGC 1183
 Qy 1204 GTGTATGGGCTCTGGTACCTCAGTTCTGACCTTGTGTTTACATCGTTATCTTCCCCAGCTG 1263

Db 1184 GTTTATACTTTATGGTATTTGGCTTCGGATTTAGTTTATTGCATTCTTTTTCCCCAGTTA 1243

Qy 1264 CTTTGTGTACTCTTTGTTAAGGGAACCAACACCTATGGGGCCGTGGCAGGTTATGTTTCT 1323
 | | | | | | | | | | | | | | | | | | | | | |

Db 1244 ACAATGGCCCTCTTTTATAAAAGAGCAAATCTTTACGGGTCGATTGCTGGATTTCAGTT 1303

Qy 1324 GGCCTCTTCCTGAGAATAACTGGAGGGGAGCCATATCTGTATCTTCAGCCCTTGATCTTC 1383
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Db 1304 GCAGTCATTCTGAGGCTCGGCGGTGGTGAACCCGCATTCGGCATTCCGCCGCTTCTGCCG 1363

Qy 1384 TACCC 1388
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Db 1364 TATCC 1368

RESULT 11

US-09-911-077A-19/c

; Sequence 19, Application US/09911077A

; Publication No. US20030114399A1

; GENERAL INFORMATION:

; APPLICANT: BLAKELY, RANDY D.

; APPLICANT: APPARSUNDARAM, SUBRAMANIAM

; APPLICANT: FERGUSON, SHAWN

; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA

; FILE REFERENCE: VBLT:008US

; CURRENT APPLICATION NUMBER: US/09/911,077A

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 119040

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (2347)..(90873)

; OTHER INFORMATION: N = A, C, G or T/U

US-09-911-077A-19

Query Match 10.4%; Score 180.8; DB 10; Length 119040;

Best Local Similarity 98.9%; Pred. No. 6.9e-42;

Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
 | | | | | | | | | | | | | | | | | | | | | |

Db 94584 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 94525

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
 | | | | | | | | | | | | | | | | | | | | | |

Db 94524 GTTGAATATGGGCTGCCTGGAGAACCAAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 94465

Qy 121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180
 | | | | | | | | | | | | | | | | | | | | | |

Db 94464 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGGT 94405

Qy 181 ACCT 184
 | | |

Db 94404 ACGT 94401

RESULT 12

US-09-911-077A-14/c

; Sequence 14, Application US/09911077A
; Publication No. US20030114399A1
; GENERAL INFORMATION:
; APPLICANT: BLAKELY, RANDY D.
; APPLICANT: APPARSUNDARAM, SUBRAMANIAM
; APPLICANT: FERGUSON, SHAWN
; TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER cDNA
; FILE REFERENCE: VBLT:008US
; CURRENT APPLICATION NUMBER: US/09/911,077A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 142299
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1305)..(127835)
; OTHER INFORMATION: N = A, C, G or T/U
US-09-911-077A-14

Query Match 10.4%; Score 180.8; DB 10; Length 142299;
Best Local Similarity 98.9%; Pred. No. 7.8e-42;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 60
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Db 64222 ATGGCTTTCCATGTGGAAGGACTGATAGCTATCATCGTGTCTACCTTCTAATTTTGCTG 64163

Qy 61 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 120
|
Db 64162 GTTGAATATGGGCTGCCTGGAGAACCAAAACAGTGGCAGCGCAGAAGAGCGCAGCGAA 64103

Qy 121 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGCT 180
|
Db 64102 GCCATCATAGTTGGTGGCCGAGATATTGGTTTATTGGTTGGTGGATTACCATGACAGGT 64043

Qy 181 ACCT 184
|||
Db 64042 ACGT 64039

RESULT 13

US-09-864-761-1838

; Sequence 1838, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1838
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009963.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3

; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
US-09-864-761-1838

Query Match 8.9%; Score 155; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.1e-36;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 741 GATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGGGTTCTCTCTTCTCCTCAGC 800
|||||
Db 266 GATGCTGGGTGGAATCCCATGGCAAGCATACTTTCAGAGGGTTCTCTCTTCTCCTCAGC 325

Qy 801 CACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGGTGCCTGGTGATGGCCATCCC 860
|||||
Db 326 CACCTATGCTCAAGTGCTGTCCTTCTGGCAGCTTTCGGGTGCCTGGTGATGGCCATCCC 385

Qy 861 AGCCATACTCATTGGGGCCATTGGAGCATCAACAG 895
|||||
Db 386 AGCCATACTCATTGGGGCCATTGGAGCATCAACAG 420

RESULT 14

US-10-027-632-120553/c

; Sequence 120553, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120553
; LENGTH: 943
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120553

Query Match 6.8%; Score 118.6; DB 15; Length 943;

Best Local Similarity 99.2%; Pred. No. 1.4e-24;
Matches 118; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 176 CAGCTACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAG 235
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Db 589 CAGCTACCTGGGTCGGAGGAGGGTATATCAATGGCACAGCTGAAGCAGTTTATGTACCAG 530

Qy 236 GTTATGGCCTAGCTTGGGCTCAGGCACCAATTGGATATTCTCTTAGTCTGATTTTAGGT 294
|||||:|||||
Db 529 GTTATGGCCTAGCTTGGGCTCAGGCACCARTGGATATTCTCTTAGTCTGATTTTAGGT 471

RESULT 15

US-09-864-761-18589

; Sequence 18589, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES

USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18589
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009963.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: gill1141884, EVALUE 5.00e-33
US-09-864-761-18589
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Query Match          4.1%; Score 72; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      824 TCCTGGCAGCTTTCGGGTGCCTGGTGGTATGGCCATCCCAGCCATACTCATTGGGGCCATTG 883
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Db      1 TCCTGGCAGCTTTCGGGTGCCTGGTGGTATGGCCATCCCAGCCATACTCATTGGGGCCATTG 60

Qy      884 GAGCATCAACAG 895
          |||||||||||
Db      61 GAGCATCAACAG 72
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Job time : 650 secs
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